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**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. §371**

SCH 1764

U.S. APPLICATION NO. (If known see 37 CFR §1.5)

09/646569

INTERNATIONAL APPLICATION NO.

PCT/DE99/00909

INTERNATIONAL FILING DATE

19 MARCH 1999

PRIORITY DATE CLAIMED

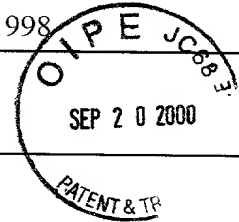
20 MARCH 1998

TITLE OF INVENTION

HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

APPLICANT(S) FOR DO/EO/US

SPECHT, Thomas, et al.



Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. §371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. §371.
3. ☐ This express request to begin national examination procedures (35 U.S.C. §371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. §371(b) and PCT Articles 22 and 39(1).
4. ☒ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. §371(c)(2))
 - a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☒ has been transmitted by the International Bureau.
 - c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☒ A translation of the International Application into English (35 U.S.C. §371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. §371(c)(3))
 - a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. ☐ have been transmitted by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. §371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. §371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. §371(c)(5)).

Items 11. to 16. below concern document(s) or information included:

11. ☐ An Information Disclosure Statement under 37 C.F.R. §§1.97 and 1.98.
12. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 C.F.R. §§3.28 and 3.31 is included.
13. ☒ A **FIRST** preliminary amendment.
 ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information: PAPER COPY OF SEQUENCE LISTING AND DISKETTE COPY

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SCH 1764

(November 1998)

IN THE UNITED STATES DESIGNATED/ELECTED OFFICE

International Application No. : PCT/DE99/00909
International Filing Date : 19 MARCH 1999
Priority Date(s) Claimed : 20 MARCH 1998
Applicant(s) (DO/EO/US) : SPECHT, Thomas, et al.

Title: HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

PRELIMINARY AMENDMENT

Commissioner for Patents
Washington, D.C. 20231

SIR:

Prior to calculating the national fee, and prior to examination in the National Phase of the above-identified International application, please amend as follows:

IN THE CLAIMS:

Claim 4, line 3, after "178" insert --of Claim 3--;
Claim 5, line 1, delete "claims 1 to 4" and insert --Claim 3--;
Claim 6, line 1, delete "claims 1 to 4" and insert --Claim 3--;
Claim 7, line 2, delete "claims 1 to 6" and insert --Claim 3--;
line 4, delete "claims 1 to 6" and insert --Claim 3--;
Claim 8, line 1, delete "claims 1 to 7" and insert --Claim 3--;
Claim 9, line 1, delete "claims 1 to 7" and insert --Claim 3--;
Claim 10, lines 1 and 2, delete "one of claims 1 to 9" and insert --Claim 3--;
Claim 11, line 2, delete "one of claims 1 to 9" and insert --Claim 3--;
Claim 13, lines 1 and 2, delete "one of claims 11 and 12" and insert --Claim 11--;
Claim 14, lines 1 and 2, delete "claims 1 to 10" and insert --Claim 3--;
Claim 16, line 3, delete "one of claims 1 to 10" and insert --Claim 3--;
Claim 18, line 1, delete "one of claims 16 or 17" and insert --Claim 16--;
Claim 19, line 2, delete "claims 16 to 18" and insert --Claim 16--;

Table 1

Claim 36, line 1, delete "claims 1 to 7" and insert --Claim 3--.

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

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SCH 1764

Human Nucleic Acid Sequences from Normal Breast Tissue

The invention relates to human nucleic acid sequences from breast tissue, which code for gene products or parts thereof, their functional genes that code at least one bioactive polypeptide and their use.

In addition, the invention relates to the polypeptides that can be obtained by way of the sequences and their use.

One of the main causes of death in women is breast cancer, for control of which new therapies are necessary. Previously used therapies, such as, e.g., chemotherapy, hormone therapy or surgical removal of tumor tissue, frequently do not result in a complete cure.

The cancer phenomenon often goes along with overexpression or underexpression of certain genes in degenerated cells, it still being unclear whether these altered expression rates are the cause or the result of the malignant transformation. Identification of these genes would be an important step for development of new therapies against cancer. Spontaneous formation of cancer is often preceded by a host of mutations. They can have the most varied effects on the expression pattern in the affected tissue, such as, e.g., underexpression or overexpression, but also expression of shortened genes. Several such changes due to these mutation cascades can ultimately lead to malignant degeneration. The complexity of these relationships makes an experimental approach very difficult.

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It has now been found that this error possibility can be reduced if all ESTs from the respective tissue type are assembled beforehand, before the expression patterns are compared to one another. Overlapping ESTs of the same gene were thus combined into longer sequences (see Figure 1, Figure 2a and Figure 3). This lengthening and thus coverage of an essentially larger gene

region in each of the respective bases are intended to largely avoid the above-described error. Since there were no existing software products for this purpose, programs for assembling genomic sections were employed, which were used modified and to which our own programs were added. A flow chart of the assembly procedure is shown in Figures 2b1-2b4.

Nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID 178, which play a role as candidate genes in breast tumors, have now been found.

Nucleic acid sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 are of special interest.

The invention thus relates to nucleic acid sequences that code a gene product or a part thereof, comprising

a) a nucleic acid sequence selected from the group of nucleic acid sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

In addition, the invention relates to a nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 or a complementary or

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allelic variant thereof and the nucleic acid sequences thereof, which have 90% to 95% homology to a human nucleic acid sequence.

The invention also relates to nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, which are expressed elevated in normal breast tissue or are expressed reduced in breast tumor tissue.

The invention further relates to nucleic acid sequences comprising a portion of the above-mentioned nucleic acid sequences in such a sufficient amount that they hybridize with sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178.

The nucleic acid sequences according to the invention generally have a length of at least 50 to 4500 bp, preferably a length of at least 150 to 4000 bp, especially a length of 450 to 3500 bp.

With the partial sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178 according to the invention, expression cassettes can also be built using current process practice, whereby on the cassette at least one of the nucleic acid sequences according to the invention is combined with at least one control or regulatory sequence generally known to one skilled in the art, such as, e.g., a suitable promoter. The sequences according to the invention can be inserted in a sense or antisense orientation.

Expression cassettes or vectors are defined as:

A control or regulatory sequence is defined as suitable promoters. Here, two preferred vectors are the pKK232-8 and the PCM7 vector. In particular, the following promoters are intended: lacI, lacZ, T3, T7, gpt, lambda P_R, trc, CMV, HSV thymidine-kinase, SV40, LTRs from retrovirus and mouse metallothionein-I.

The expression cassettes are likewise the subject matter of this invention.

The invention also relates to the use of the nucleic acid sequences according to the invention and the gene fragments that can be obtained from use.

The nucleic acid sequences according to the invention can be moved with suitable vectors into host cells, in which as the

heterologous part, the genetic information which is contained on the nucleic acid fragments and which is expressed is located.

The host cells containing the nucleic acid fragments are likewise the subject matter of this invention.

Suitable host cells are, e.g., prokaryotic cell systems such as E. coli or eukaryotic cell systems such as animal or human cells or yeasts.

The nucleic acid sequences according to the invention can be used in the sense or antisense form.

Production of polypeptides or their fragments is done by cultivation of the host cells according to current cultivation methods and subsequent isolation and purification of the peptides or fragments, likewise using current methods. The invention further relates to nucleic acid sequences, which code at least a partial sequence of a bioactive polypeptide.

This invention further relates to polypeptide partial sequences, so-called ORF (open-reading-frame)-peptides according to the sequence protocols Seq. ID Nos. 77-85, 87, 88, 90, 91, 93, 95-108, 112-117, 119, 122, 124-126, 132, 133, 135, 137-160 and 179-209.

The invention further relates to the polypeptide sequences that have at least 80% homology, especially 90% homology to the polypeptide partial sequences of Seq. ID Nos. 77-85, 87, 88, 90, 91, 93, 95-108, 112-117, 119, 122, 124-126, 132, 133, 135, 137-160 and 179-209 according to the invention.

The invention also relates to antibodies that are directed against a polypeptide or a fragment thereof and that are coded by

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The invention also relates to genomic genes, their exon and intron structures and their splice variants that can be obtained from cDNAs of sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq.

ID No. 161 to Seq. ID No. 178, and their use together with suitable regulatory elements, such as suitable promoters and/or enhancers.

With the nucleic acids according to the invention (cDNA sequences), genomic BAC, PAC and Cosmid libraries are screened and specifically human clones are isolated via complementary base pairing (hybridization). The BAC, PAC and Cosmid clones isolated in this way are hybridized using fluorescence-in-situ hybridization on metaphase chromosomes and the corresponding chromosome sections on which the corresponding genomic genes lie are identified. BAC, PAC and Cosmid clones are sequenced in order to clarify the corresponding genomic genes in their complete structure (promoters, enhancers, silencers, exons and introns). BAC, PAC and Cosmid clones can be used as independent molecules for gene transfer (see Figure 5).

The invention also relates to BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 179, for use as vehicles for gene transfer.

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Nucleic acids= Nucleic acids in this invention are defined as:

ORF = Open Reading Frame, a defined sequence of amino acids which can be derived from the cDNA sequence.

Singleton = A contig that contains only one sequence.

N = selectively the nucleotide A, T, G or C.

Explanation of the alignment parameters

maximum pads per read = maximum number of insertions

Explanation of Figures

Figure 2a shows the principle of EST assembling

Figures 2b1-2b4 show the entire principle of EST assembling

- Figure 3 shows the in-silico subtraction of gene expression in various tissues
- Figure 4a shows the determination of tissue-specific expression via electronic Northern
- Figure 4b shows the electronic Northern
- Figure 5 shows the isolation of genomic BAC and PAC clones.

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The following examples explain the production of the nucleic acid sequences according to the invention without limiting the invention to these examples and nucleic acid sequences.

Example 1

Search for tumor-related candidate genes

First, all ESTs of the corresponding tissue from the LifeSeq database (from October 1997) were extracted. They were then assembled by means of the GAP4 program of the Staden package with the parameters 0% mismatch, 8 pads per read and a minimal match of 20. The sequences (fails) not recorded in the GAP4 database were assembled first at 1% mismatch and then again at 2% mismatch with the database. Consensus sequences were computed from the contigs of the database that consisted of more than one sequence. The singletons of the database, which consisted of only one sequence, were re-assembled at 2% mismatch with the sequences not recorded in the GAP4 database. In turn, the consensus sequences were determined for the contigs. All other ESTs were re-assembled at 4% mismatch. The consensus sequences were extracted once again and finally assembled with the previous consensus sequences and the singletons and the sequences not recorded in the database at 4% mismatch. The consensus sequences were formed and used with the singletons and fails as the initial basis for tissue comparisons. This procedure ensured that among the parameters used, all sequences represented gene regions independent of one another.

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Figures 2b1-2b4 illustrate the lengthening of the breast tissue ESTs.

The sequences of the respective tissue assembled in this way were then compared to one another by means of the same program (Figure 3). To do this, first all sequences of the first tissue were input into the database. (It was therefore important that they were independent of one another).

Then, all sequences of the second tissue were compared to all those of the first. The result was sequences that were specific to the first or the second tissue as well as those which occurred in both. In the latter, the ratio of the frequency of occurrence in the respective tissue was evaluated. All programs pertaining to the evaluation of the assembled sequences were themselves developed.

All sequences that occurred more than four times in respectively one of the compared tissues and all that occurred at least five times as often in one of the two tissues were further studied. These sequences were subjected to an electronic Northern (see Example 2.1), by which the distribution in all tumor and normal tissues was studied (see Figure 4a and Figure 4b). The relevant candidates were then lengthened using all Incyte ESTs and all ESTs of public databases (see Example 3). Then, the sequences and their translation into possible proteins were compared to all nucleotide and protein databases and were studied for possible regions that code for proteins.

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Example 2**Algorithm for identification and lengthening of partial cDNA sequences with altered expression pattern**

An algorithm for finding overexpressed or underexpressed genes will be explained below. The individual steps are also summarized in a flow chart for the sake of clarity (see Figure 4b).

2.1. Electronic Northern Blot

By means of a standard program for homology search, e.g., BLAST (Altschul, S. F.; Gish, W.; Miller, W.; Myers, E. W. and Lipman, D. J. (1990) J. Mol. Biol. 215, 403-410), BLAST2 (Altschul, S. F.; Madden, T. L.; Schäffer, A. A.; Zhang, J.; Zhang, Z.; Miller, W., and Lipman, D. J. (1997) Nucleic Acids Research 25 3389-3402) or FASTA (Pearson, W. R. and Lipman, D. J. (1988) Proc. Natl. Acad. Sci. USA 85 2444-2448), the homologous sequences in various EST libraries (private or public) arranged by tissues are determined for a partial DNA sequence S, e.g., an individual EST or a contig of ESTs. The (relative or absolute) tissue-specific occurrence frequencies of this partial sequence S which were determined in this way are called electronic Northern Blots.

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2.1.1

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 39 was found which occurs 21x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to human alpha-B-crystalline.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 39

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0139	0.0102	1.3639 0.7332
Breast	0.0919	0.0044	21.0995 0.0474
Ovary	0.0091	0.0104	0.8765 1.1409
Endocrine tissue	0.0146	0.0027	5.3582 0.1866
Gastrointestinal	0.0213	0.0048	4.4784 0.2233
Brain	0.1941	0.1358	1.4296 0.6995
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0995	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.2405	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0324	0.0142	2.2824 0.4381
Stomach-esophagus	0.0097	0.0230	0.4200 2.3811
Muscle-skeleton	0.1456	0.0180	8.0893 0.1236
Kidneys	0.0327	0.1643	0.1990 5.0254
Pancreas	0.0038	0.0055	0.6857 1.4584
Penis	0.0539	0.0000	undef 0.0000
Prostate	0.0238	0.0149	1.5980 0.6258
Uterus	0.0363	0.0356	1.0212 0.9793
Breast hyperplasia	0.0291		
Small intestine	0.0156		
Prostatic hyperplasia	0.0119		
Seminal vesicles	0.0178		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.1063
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0419

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.2925
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0379
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0874
Testicles	0.0234
Lungs	0.0082
Nerves	0.0462
Prostate	0.0321
Sensory organs	0.0542

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2.1.2

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 41 was found which occurs 15x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to human extracellular protein S1-5.

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 41

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0186	0.0026	7.2739 0.1375
Breast	0.0666	0.0044	15.2895 0.0654
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0347	0.0436	0.7954 1.2573
Gastrointestinal	0.0078	0.0095	0.8143 1.2281
Brain	0.0288	0.0077	3.7599 0.2660
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0497	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0498	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0125	0.0095	1.3168 0.7594
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0086	0.0420	0.2039 4.9036
Kidneys	0.0178	0.0000	undef 0.0000
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000	0.0000	undef undef
Small intestine	0.0799		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0089		
White blood cells	0.0000		
	0.0070		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0313
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0068
Endocrine tissue	0.0245
Fetal	0.0099
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0000
Nerves	0.0120
Prostate	0.0000
Sensory organs	0.0000

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2.1.3

Analogously to the procedure described under 2.1, the sequence Seq. ID No. 42 was found which occurs 12x more heavily in normal breast tissue than in tumor tissue.

The possible function of this gene region relates to secreted "frizzled-related protein."

The result is as follows:

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Electronic Northern for SEQ. ID NO.: 42

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0511	0.0026	20.00330.0500
Breast	0.0533	0.0044	12.23160.0818
Ovary	0.0030	0.0078	0.3895 2.5671
Endocrine tissue	0.0128	0.0027	4.6885 0.2133
Gastrointestinal	0.0039	0.0000	undef 0.0000
Brain	0.0059	0.0099	0.6021 1.6609
Hematopoietic	0.0014	0.0000	undef 0.0000
Skin	0.0348	0.0000	undef 0.0000
Hepatic	0.0149	0.0065	2.2954 0.4356
Heart	0.0085	0.0000	undef 0.0000
Testicles	0.0061	0.0117	0.5224 1.9144
Lungs	0.0025	0.0000	undef 0.0000
Stomach-esophagus	0.0097	0.0000	undef 0.0000
Muscle-skeleton	0.0120	0.0240	0.4996 2.0015
Kidneys	0.0535	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0090	0.0000	undef 0.0000
Prostate	0.0048	0.0085	0.5593 1.7879
Uterus	0.0231	0.0000	undef 0.0000
Breast hyperplasia	0.1126		
Small intestine	0.0156		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0178		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0615
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0573
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0117
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0161
Sensory organs	0.0000
	0.0000

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In an analogous procedure, the following Northernblots were also found:

Electronic Northern Blot for SEQ. ID. NO: 1

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0139	0.0179	0.7793 1.2831
	0.0160	0.0022	7.3390 0.1363
Bladder	0.0030	0.0052	0.5843 1.7114
Breast	0.0036	0.0109	0.3349 2.9861
Ovary	0.0039	0.0238	0.1629 6.1405
Endocrine tissue	0.0102	0.0088	1.1612 0.8612
Gastrointestinal	0.0070	0.0000	undef 0.0000
Brain	0.0050	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0065	0.0000 undef
Skin	0.0011	0.0137	0.0771 12.9744
Hepatic	0.0122	0.0117	1.0447 0.9572
Heart	0.0037	0.0071	0.5267 1.8986
Testicles	0.0000	0.0000	undef undef
Lungs	0.0103	0.0120	0.8565 1.1675
Stomach-esophagus	0.0030	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0110	0.0000 undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0048	0.0128	0.3729 2.6818
Penis	0.0066	0.0000	undef 0.0000
Prostate	0.0109		
Uterus	0.0000		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0061		
White blood cells			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0154
Brain	0.0313
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0371
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES % frequency

Breast	0.0000
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0078
Lungs	0.0000
Nerves	0.0020
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 2

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0000	0.0052	0.0000 undef
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0143	0.0000 undef
Gastrointestinal	0.0093	0.0044	2.1288 0.4698
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0032	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0017	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0071	0.0064	1.1186 0.8939
Prostate	0.0050	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0044		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0205
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0082
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 3

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0046	0.0000	undef 0.0000
Breast	0.1066	0.0065	16.308 0.0613
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0000	0.0000	undef undef
Brain	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0056	0.0000	undef 0.0000
Skin	0.0448	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0095	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0059	0.0000	undef 0.0000
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus	0.0000	0.0021	0.0000 undef
Breast hyperplasia	0.0000	0.0000	undef undef
Small intestine	0.0400		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 4

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0133	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0054	0.3349	2.9861
Endocrine tissue	0.0078	0.0048	1.6285	0.6141
Gastrointestinal	0.0034	0.0022	1.5482	0.6459
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0099	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0025	0.0024	1.0534	0.9493
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0060	0.0000	undef
Muscle-skeleton	0.0089	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0024	0.0021	1.1186	0.8939
Prostate	0.0033	0.0214	0.1547	6.4632
Uterus	0.0073			
Breast hyperplasia	0.0000			
Small intestine	0.0059			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0155

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Electronic Northern Blot for SEQ. ID. NO: 5

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0790	0.0435	1.8185 0.5499
Bladder	0.0187	0.0022	8.5621 0.1168
Breast	0.0122	0.0000	undef 0.0000
Ovary	0.0000	0.0027	0.0000 undef
Endocrine tissue	0.0329	0.0000	undef 0.0000
Gastrointestinal	0.0085	0.0033	2.5804 0.3875
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0212	0.0000	undef 0.0000
Heart	0.0122	0.0117	1.0447 0.9572
Testicles	0.0025	0.0071	0.3511 2.8478
Lungs	0.1159	0.0383	3.0238 0.3307
Stomach-esophagus	0.0240	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0898	0.0000	undef 0.0000
Penis	0.0262	0.0192	1.3672 0.7314
Prostate	0.0099	0.0427	0.2321 4.3088
Uterus	0.0291		
Breast hyperplasia	0.0530		
Small intestine	0.0178		
Prostatic hyperplasia	0.0445		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 10

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0107	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0027	0.0000	undef
Endocrine tissue	0.0039	0.0000	undef	0.0000
Gastrointestinal	0.0025	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0099	0.0000	undef	0.0000
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0021	0.0000	undef	0.0000
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0025	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0017	0.0000	undef	0.0000
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0476
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0080
Prostate	0.0000
Sensory organs	0.0000

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	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0067	0.0000	undef	0.0000
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0073	0.0054	1.3396	0.7465
Endocrine tissue	0.0000	0.0048	0.0000	undef
Gastrointestinal	0.0144	0.0110	1.3160	0.7599
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0065	0.0000	undef
Hepatic	0.0042	0.0000	undef	0.0000
Heart	0.0000	0.0117	0.0000	undef
Testicles	0.0025	0.0095	0.2634	3.7971
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0034	0.0060	0.5710	1.7513
Muscle-skeleton	0.0030	0.0000	undef	0.0000
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0060	0.0000	undef	0.0000
Penis	0.0048	0.0149	0.3196	3.1288
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0000			
Breast hyperplasia	0.0093			
Small intestine	0.0149			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0026			

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0000
Ovary-uterus	0.0091
Endocrine tissue	0.0245
Fetal	0.0029
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0080
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 12

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0093	0.0022	4.2811	0.2336
Breast	0.0000	0.0104	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0024	1.5801	0.6329
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0030	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0017	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0035
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0000
Sensory organs	0.0232

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Electronic Northern Blot for SEQ. ID. NO: 13

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0000	undef	0.0000
	0.0080	0.0022	3.6695	0.2725
Bladder	0.0091	0.0000	undef	0.0000
Breast	0.0128	0.0054	2.3442	0.4266
Ovary	0.0000	0.0048	0.0000	undef
Endocrine tissue	0.0042	0.0022	1.9353	0.5167
Gastrointestinal	0.0014	0.0000	undef	0.0000
Brain	0.0050	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0032	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0012	0.0024	0.5267	1.8986
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0051	0.0060	0.8565	1.1675
Stomach-esophagus	0.0030	0.0137	0.2171	4.6066
Muscle-skeleton	0.0000	0.0055	0.0000	undef
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0048	0.0000	undef	0.0000
Penis	0.0083	0.0356	0.2321	4.3088
Prostate	0.0073			
Uterus	0.0125			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0044			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0092
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0164
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0128
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 14

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0051	0.9092 1.0998
Bladder	0.0120	0.0000	undef 0.0000
Breast	0.0000	0.0026	0.0000 undef
Ovary	0.0036	0.0027	1.3396 0.7465
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0017	0.0022	0.7741 1.2918
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0042	0.0000	undef 0.0000
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0086	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0000	0.0110	0.0000 undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0095	0.0043	2.2373 0.4470
Prostate	0.0017	0.0071	0.2321 4.3088
Uterus	0.0073		
Breast hyperplasia	0.0062		
Small intestine	0.0030		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0026		
White blood cells			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0000
Hematopoietic	0.0285
Skin-muscle	0.0291
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 15

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0000	undef	0.0000
Bladder	0.0187	0.0022	8.5621	0.1168
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0076	0.0011	6.9669	0.1435
Brain	0.0042	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0137	0.3854	2.5949
Heart	0.0000	0.0000	undef	undef
Testicles	0.0025	0.0071	0.3511	2.8478
Lungs	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0090	0.0000	undef	0.0000
Penis	0.0024	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0036			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0030			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0125
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 16

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0051	1.8185	0.5499
Breast	0.0160	0.0000	undef	0.0000
Ovary	0.0091	0.0000	undef	0.0000
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0017	0.0011	1.5482	0.6459
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0021	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0060	0.5710	1.7513
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0090	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0099	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0558

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 18

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0232	0.0026	9.0924 0.1100
Breast	0.0306	0.0044	7.0332 0.1422
Ovary	0.0030	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0027	0.0000 undef
Gastrointestinal	0.0252	0.0000	undef 0.0000
Brain	0.0017	0.0011	1.5482 0.6459
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0249	0.0000	undef 0.0000
Hepatic	0.0000	0.0065	0.0000 undef
Heart	0.0148	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0037	0.0024	1.5801 0.6329
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0274	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0057	0.0000	undef 0.0000
Penis	0.0120	0.0267	0.4492 2.2260
Prostate	0.0095	0.0000	undef 0.0000
Uterus	0.0132	0.0000	undef 0.0000
Breast hyperplasia	0.0291		
Small intestine	0.0062		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0118		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 19

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0093	0.0000	undef	0.0000
Breast	0.0120	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0054	0.0000	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0017	0.0011	1.5482	0.6459
Hematopoietic	0.0014	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0074	0.0275	0.2698	3.7070
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0025	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0048	0.0000	undef	0.0000
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0073			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0140
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

000260" 6954950

Electronic Northern Blot for SEQ. ID. NO: 21

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0000	0.0000	undef undef
Breast	0.0227	0.0044	5.1984 0.1924
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0019	0.0095	0.2036 4.9124
Brain	0.0017	0.0000	undef 0.0000
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0064	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0012	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0153	0.0000 undef
Muscle-skeleton	0.0017	0.0060	0.2855 3.5025
Kidneys	0.0059	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000	0.0000	undef undef
Small intestine	0.0036		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		
	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0544
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0064
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 22

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0133	0.0000	undef 0.0000
Breast	0.0000	0.0000	undef undef
Ovary	0.0018	0.0000	undef 0.0000
Endocrine tissue	0.0058	0.0000	undef 0.0000
Gastrointestinal	0.0000	0.0033	0.0000 undef
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lungs	0.0050	0.0000	undef 0.0000
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0034	0.0060	0.5710 1.7513
Kidneys	0.0030	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Prostate	0.0024	0.0064	0.3729 2.6818
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0109		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0068
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260 6959450

Electronic Northern Blot for SEQ. ID. NO: 23

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0026	1.8185	0.5499
	0.0133	0.0022	6.1158	0.1635
Bladder	0.0000	0.0000	undef	undef
Breast	0.0036	0.0027	1.3396	0.7465
Ovary	0.0097	0.0000	undef	0.0000
Endocrine tissue	0.0008	0.0033	0.2580	3.8754
Gastrointestinal	0.0014	0.0000	undef	0.0000
Brain	0.0050	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0011	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0037	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0069	0.0060	1.1420	0.8756
Stomach-esophagus	0.0149	0.0000	undef	0.0000
Muscle-skeleton	0.0038	0.0000	undef	0.0000
Kidneys	0.0030	0.0000	undef	0.0000
Pancreas	0.0024	0.0000	undef	0.0000
Penis	0.0033	0.0071	0.4642	2.1544
Prostate	0.0036			
Uterus	0.0000			
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0118			
Sensory organs	0.0000			
White blood cells				

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0490
Fetal	0.0198
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0192
Sensory organs	0.0000

000260" 69594360

Electronic Northern Blot for SEQ. ID. NO: 24

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0139	0.0153	0.9092 1.0998
Breast	0.0173	0.0022	7.9505 0.1258
Ovary	0.0000	0.0026	0.0000 undef
Endocrine tissue	0.0018	0.0027	0.6698 1.4930
Gastrointestinal	0.0058	0.0000	undef 0.0000
Brain	0.0085	0.0142	0.5955 1.6794
Hematopoietic	0.0042	0.0000	undef 0.0000
Skin	0.0298	0.0000	undef 0.0000
Hepatic	0.0050	0.0000	undef 0.0000
Heart	0.0106	0.0000	undef 0.0000
Testicles	0.0061	0.0000	undef 0.0000
Lungs	0.0037	0.0071	0.5267 1.8986
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0103	0.0000	undef 0.0000
Kidneys	0.0178	0.0068	2.6050 0.3839
Pancreas	0.0019	0.0055	0.3428 2.9168
Penis	0.0000	0.0533	0.0000 undef
Prostate	0.0048	0.0021	2.2373 0.4470
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0327		
Small intestine	0.0062		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0089		
Sensory organs	0.0118		
White blood cells	0.0244		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0114
Skin-muscle	0.0065
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0000

00000 " 69594960

Electronic Northern Blot for SEQ. ID. NO: 25

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0651	0.0204	3.1823 0.3142
Bladder	0.0400	0.0065	6.1158 0.1635
Breast	0.0213	0.0026	8.1803 0.1222
Ovary	0.0109	0.0163	0.6698 1.4930
Endocrine tissue	0.0271	0.0000	undef 0.0000
Gastrointestinal	0.0119	0.0066	1.8062 0.5536
Brain	0.0196	0.0000	undef 0.0000
Hematopoietic	0.0199	0.0000	undef 0.0000
Skin	0.0050	0.0065	0.7651 1.3069
Hepatic	0.0286	0.0000	undef 0.0000
Heart	0.0061	0.0000	undef 0.0000
Testicles	0.0174	0.0047	3.6870 0.2712
Lungs	0.0193	0.0077	2.5198 0.3968
Stomach-esophagus	0.0206	0.0120	1.7130 0.5838
Muscle-skeleton	0.0089	0.0068	1.3025 0.7678
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0599	0.0000	undef 0.0000
Penis	0.0214	0.0362	0.5922 1.6886
Prostate	0.0430	0.0000	undef 0.0000
Uterus	0.0254		
Breast hyperplasia	0.0343		
Small intestine	0.0297		
Prostatic hyperplasia	0.0356		
Seminal vesicles	0.0118		
Sensory organs	0.0000		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0197
Heart-blood vessels	0.0041
Lungs	0.0185
Kidneys	0.0309
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0816
Ovary-uterus	0.0160
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0040
Prostate	0.0385
Sensory organs	0.0000

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 26

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0000	undef	undef
Breast	0.0187	0.0022	8.5621	0.1168
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0050	0.0000	undef	0.0000
Hepatic	0.0000	0.0065	0.0000	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0077	0.0000	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0110	0.0000	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000	0.0000	undef	undef
Small intestine	0.0036			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 28

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0102	0.9092 1.0998
Bladder	0.0267	0.0087	3.0579 0.3270
Breast	0.0091	0.0156	0.5843 1.7114
Ovary	0.0128	0.0082	1.5628 0.6399
Endocrine tissue	0.0174	0.0095	1.8321 0.5458
Gastrointestinal	0.0127	0.0153	0.8294 1.2057
Brain	0.0042	0.0000	undef 0.0000
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0149	0.0194	0.7651 1.3069
Hepatic	0.0085	0.0137	0.6166 1.6218
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0212	0.0189	1.1193 0.8934
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0240	0.0120	1.9985 0.5004
Muscle-skeleton	0.0119	0.0000	undef 0.0000
Kidneys	0.0114	0.0166	0.6857 1.4584
Pancreas	0.0090	0.0267	0.3369 2.9680
Penis	0.0191	0.0298	0.6392 1.5644
Prostate	0.0149	0.0000	undef 0.0000
Uterus	0.0109		
Breast hyperplasia	0.0093		
Small intestine	0.0178		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0113		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0247
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0160
Endocrine tissue	0.0490
Fetal	0.0245
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0164
Nerves	0.0211
Prostate	0.0256
Sensory organs	0.0000

000260" 69594660

Electronic Northern Blot for SEQ. ID. NO: 29

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0179	0.0000 undef
Bladder	0.0466	0.0131	3.5675 0.2803
Breast	0.0304	0.0130	2.3372 0.4279
Ovary	0.0237	0.0300	0.7916 1.2633
Endocrine tissue	0.0136	0.0238	0.5700 1.7544
Gastrointestinal	0.0424	0.0263	1.6127 0.6201
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0348	0.0000	undef 0.0000
Skin	0.0198	0.0065	3.0606 0.3267
Hepatic	0.0265	0.0687	0.3854 2.5949
Heart	0.0244	0.0000	undef 0.0000
Testicles	0.0336	0.0236	1.4221 0.7032
Lungs	0.0483	0.0307	1.5749 0.6350
Stomach-esophagus	0.0154	0.0240	0.6424 1.5567
Muscle-skeleton	0.0119	0.0274	0.4342 2.3033
Kidneys	0.0133	0.0166	0.8000 1.2501
Pancreas	0.0359	0.0000	undef 0.0000
Penis	0.0095	0.0170	0.5593 1.7879
Prostate	0.0132	0.0000	undef 0.0000
Uterus	0.0291		
Breast hyperplasia	0.0187		
Small intestine	0.0149		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0118		
Sensory organs	0.0052		
White blood cells			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0277
Brain	0.0188
Hematopoietic	0.0236
Heart-blood vessels	0.0368
Lungs	0.0407
Kidneys	0.0309
Prostate	0.0249
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0228
Endocrine tissue	0.0245
Fetal	0.0280
Gastrointestinal	0.0122
Hematopoietic	0.0171
Skin-muscle	0.0648
Testicles	0.0156
Lungs	0.0246
Nerves	0.0221
Prostate	0.0192
Sensory organs	0.1393

000260" 69594960

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0093	0.0026	3.6370	0.2750
Bladder	0.0040	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0036	0.0082	0.4465	2.2395
Endocrine tissue	0.0019	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0120	0.0000	undef
Brain	0.0028	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0053	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0000	undef	0.0000
Lungs	0.0193	0.0077	2.5198	0.3968
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0019	0.0055	0.3428	2.9168
Pancreas	0.0030	0.0000	undef	0.0000
Penis	0.0048	0.0085	0.5593	1.7879
Prostate	0.0033	0.0000	undef	0.0000
Uterus	0.0073			
Breast hyperplasia	0.0062			
Small intestine	0.0000			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0136
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0087
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0000
Nerves	0.0040
Prostate	0.0128
Sensory organs	0.0000

Electronic Northern Blot for SEQ. ID. NO: 31

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0026	3.6370 0.2750
Bladder	0.0293	0.0087	3.3637 0.2973
Breast	0.0091	0.0156	0.5843 1.7114
Ovary	0.0091	0.0054	1.6745 0.5972
Endocrine tissue	0.0155	0.0190	0.8143 1.2281
Gastrointestinal	0.0008	0.0077	0.1106 9.0427
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0249	0.0000	undef 0.0000
Skin	0.0050	0.0194	0.2550 3.9208
Hepatic	0.0053	0.0550	0.0963 10.3795
Heart	0.0000	0.0000	undef undef
Testicles	0.0075	0.0071	1.0534 0.9493
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0188	0.0060	3.1406 0.3184
Muscle-skeleton	0.0119	0.0000	undef 0.0000
Kidneys	0.0095	0.0276	0.3428 2.9168
Pancreas	0.0120	0.0000	undef 0.0000
Penis	0.0119	0.0128	0.9322 1.0727
Prostate	0.0116	0.0000	undef 0.0000
Uterus	0.0145		
Breast hyperplasia	0.0093		
Small intestine	0.0059		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0470		
Sensory organs	0.0009		
White blood cells			

	FETUS % freq.
Development	0.0154
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0164
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0000

	STANDARDIZED/SUBTRACTED LIBRARIES % frequency
Breast	0.0068
Ovary-uterus	0.0183
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0192
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 32

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0139	0.0077	1.8185 0.5499
Bladder	0.0227	0.0044	5.1984 0.1924
Breast	0.0030	0.0156	0.1948 5.1343
Ovary	0.0109	0.0054	2.0093 0.4977
Endocrine tissue	0.0136	0.0143	0.9500 1.0527
Gastrointestinal	0.0059	0.0033	1.8062 0.5536
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0064	0.0137	0.4624 2.1624
Heart	0.0366	0.0000	undef 0.0000
Testicles	0.0050	0.0000	undef 0.0000
Lungs	0.0000	0.0307	0.0000 undef
Stomach-esophagus	0.0120	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0038	0.0055	0.6857 1.4584
Pancreas	0.0210	0.0000	undef 0.0000
Penis	0.0024	0.0106	0.2237 4.4697
Prostate	0.0050	0.0000	undef 0.0000
Uterus	0.0073		
Breast hyperplasia	0.0218		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0035		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0037
Kidneys	0.0000
Prostate	0.0249
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0272
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0285
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0164
Nerves	0.0100
Prostate	0.0256
Sensory organs	0.0000

000260" 69594650

Electronic Northern Blot for SEQ. ID. NO: 33

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0126	0.7274 1.3748
	0.0200	0.0044	4.5868 0.2180
Bladder	0.0091	0.0078	1.1686 0.8557
Breast	0.0018	0.0191	0.0957 10.4512
Ovary	0.0116	0.0000	undef 0.0000
Endocrine tissue	0.0110	0.0197	0.5591 1.7887
Gastrointestinal	0.0070	0.0000	undef 0.0000
Brain	0.0099	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0021	0.0137	0.1541 6.4872
Hepatic	0.0061	0.0117	0.5224 1.9144
Heart	0.0075	0.0118	0.6321 1.5821
Testicles	0.0193	0.0000	undef 0.0000
Lungs	0.0017	0.0240	0.0714 14.0102
Stomach-esophagus	0.0149	0.0000	undef 0.0000
Muscle-skeleton	0.0019	0.0055	0.3428 2.9168
Kidneys	0.0060	0.0000	undef 0.0000
Pancreas	0.0238	0.0192	1.2429 0.8046
Penis	0.0116	0.0000	undef 0.0000
Prostate	0.0036		
Uterus	0.0125		
Breast hyperplasia	0.0059		
Small intestine	0.0178		
Prostatic hyperplasia	0.0118		
Seminal vesicles	0.0061		
Sensory organs			
White blood cells			

FETUS
% freq.

	0.0000
Development	0.0092
Gastrointestinal	0.0000
Brain	0.0157
Hematopoietic	0.0000
Heart-blood vessels	0.0074
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0136
Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0192
Fetal	0.0000
Gastrointestinal	0.0114
Hematopoietic	0.0097
Skin-muscle	0.0234
Testicles	0.0000
Lungs	0.0131
Nerves	0.0064
Prostate	0.0000
Sensory organs	

000260" 69544950

Electronic Northern Blot for SEQ. ID. NO: 34

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0147	0.0022	6.7274	0.1486
Ovary	0.0091	0.0052	1.7529	0.5705
Endocrine tissue	0.0000	0.0027	0.0000	undef
Gastrointestinal	0.0000	0.0048	0.0000	undef
Brain	0.0008	0.0000	undef	0.0000
Hematopoietic	0.0056	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0011	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0019	0.0000	undef	0.0000
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0033	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0000

000260" 69994960

Electronic Northern Blot for SEQ. ID. NO: 35

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0227	0.0022	10.3969	0.0962
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0017
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 36

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0325	0.0077	4.2431 0.2357
Breast	0.0386	0.0065	5.9119 0.1691
Ovary	0.0122	0.0000	undef 0.0000
Endocrine tissue	0.0036	0.0027	1.3396 0.7465
Gastrointestinal	0.0058	0.0048	1.2214 0.8187
Brain	0.0110	0.0033	3.3545 0.2981
Hematopoietic	0.0140	0.0000	undef 0.0000
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0099	0.0065	1.5303 0.6535
Heart	0.0085	0.0000	undef 0.0000
Testicles	0.0122	0.0000	undef 0.0000
Lungs	0.0112	0.0000	undef 0.0000
Stomach-esophagus	0.0193	0.0230	0.8399 1.1905
Muscle-skeleton	0.0137	0.0000	undef 0.0000
Kidneys	0.0000	0.0068	0.0000 undef
Pancreas	0.0019	0.0110	0.1714 5.8337
Penis	0.0120	0.0000	undef 0.0000
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0165	0.0071	2.3208 0.4309
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0544
Ovary-uterus	0.0114
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0122
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0060
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 37

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0077	0.6062	1.6497
Bladder	0.1053	0.0131	8.0525	0.1242
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0059	0.0000	undef	0.0000
Brain	0.0084	0.0000	undef	0.0000
Hematopoietic	0.0348	0.0000	undef	0.0000
Skin	0.0099	0.0000	undef	0.0000
Hepatic	0.0201	0.0000	undef	0.0000
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0012	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0223	0.0240	0.9279	1.0777
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0019	0.0000	undef	0.0000
Pancreas	0.0120	0.0000	undef	0.0000
Penis	0.0024	0.0043	0.5593	1.7879
Prostate	0.0083	0.0000	undef	0.0000
Uterus	0.0618			
Breast hyperplasia	0.0093			
Small intestine	0.0000			
Prostatic hyperplasia	0.0178			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.1632
Ovary-uterus	0.0000
Endocrine tissue	0.0490
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 38

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0227	0.0044	5.1984 0.1924
Breast	0.0000	0.0052	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0039	0.0048	0.8143 1.2281
Gastrointestinal	0.0000	0.0099	0.0000 undef
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0085	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0037	0.0047	0.7901 1.2657
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0154	0.0060	2.5696 0.3892
Muscle-skeleton	0.0000	0.0068	0.0000 undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0191	0.0043	4.4745 0.2235
Prostate	0.0017	0.0427	0.0387 25.8527
Uterus	0.0036		
Breast hyperplasia	0.0125		
Small intestine	0.0089		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

	0.0000
Development	0.0031
Gastrointestinal	0.0063
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0185
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0068
Breast	0.0000
Ovary-uterus	0.0012
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0082
Lungs	0.0020
Nerves	0.0128
Prostate	0.0000
Sensory organs	

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 40

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0325	0.0051	6.3647 0.1571
Breast	0.0267	0.0065	4.0772 0.2453
Ovary	0.0030	0.0026	1.1686 0.8557
Endocrine tissue	0.0146	0.0000	undef 0.0000
Gastrointestinal	0.0039	0.0095	0.4071 2.4562
Brain	0.0068	0.0307	0.2212 4.5213
Hematopoietic	0.0028	0.0378	0.0739 13.5274
Skin	0.0149	0.0000	undef 0.0000
Hepatic	0.0198	0.0129	1.5303 0.6535
Heart	0.1303	0.3299	0.3950 2.5316
Testicles	0.0183	0.0351	0.5224 1.9144
Lungs	0.0174	0.0118	1.4748 0.6781
Stomach-esophagus	0.0097	0.0460	0.2100 4.7622
Muscle-skeleton	0.0188	0.0300	0.6281 1.5921
Kidneys	0.0119	0.0479	0.2481 4.0308
Pancreas	0.0057	0.0055	1.0285 0.9723
Penis	0.0180	0.0267	0.6739 1.4840
Prostate	0.0143	0.0021	6.7118 0.1490
Uterus	0.0149	0.0000	undef 0.0000
Breast hyperplasia	0.0327		
Small intestine	0.0093		
Prostatic hyperplasia	0.0208		
Seminal vesicles	0.0000		
Sensory organs	0.1058		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0977

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0032
Testicles	0.0000
Lungs	0.0246
Nerves	0.0090
Prostate	0.0000
Sensory organs	0.0852

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 43

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0253	0.0044	5.8100 0.1721
Breast	0.0152	0.0338	0.4495 2.2249
Ovary	0.0109	0.0054	2.0093 0.4977
Endocrine tissue	0.0097	0.0000	undef 0.0000
Gastrointestinal	0.0136	0.0044	3.0964 0.3230
Brain	0.0098	0.0000	undef 0.0000
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0021	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0062	0.0024	2.6336 0.3797
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0051	0.0000	undef 0.0000
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0095	0.0064	1.4915 0.6705
Prostate	0.0083	0.0000	undef 0.0000
Uterus	0.0036		
Breast hyperplasia	0.0093		
Small intestine	0.0089		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0096		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0123
Brain	0.0188
Hematopoietic	0.0079
Heart-blood vessels	0.0082
Lungs	0.0111
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0099
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0000
Nerves	0.0070
Prostate	0.0064
Sensory organs	0.0000

000260" 69594950

Electronic Northern Blot for SEQ. ID. NO: 45

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0200	0.0022	9.1737	0.1090
Breast	0.0000	0.0026	0.0000	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0056	0.0000	undef	0.0000
Hematopoietic	0.0249	0.0000	undef	0.0000
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0064	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0038	0.0055	0.6857	1.4584
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0254			
Small intestine	0.0125			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0009			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 47

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0051	0.0000	undef
	0.0133	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0000	0.0000	undef	undef
Ovary	0.0019	0.0000	undef	0.0000
Endocrine tissue	0.0017	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0062	0.0000	undef	0.0000
Lungs	0.0193	0.0000	undef	0.0000
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0120	0.0000	undef	0.0000
Prostate	0.0024	0.0021	1.1186	0.8939
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0031			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
Breast	0.0068
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0006
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 48

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0186	0.0077	2.4246	0.4124
Bladder	0.0133	0.0000	undef	0.0000
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0036	0.0027	1.3396	0.7465
Endocrine tissue	0.0019	0.0000	undef	0.0000
Gastrointestinal	0.0017	0.0033	0.5161	1.9377
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0149	0.0000	undef	0.0000
Skin	0.0149	0.0000	undef	0.0000
Hepatic	0.1494	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0162	0.0000	undef	0.0000
Lungs	0.0097	0.0000	undef	0.0000
Stomach-esophagus	0.0394	0.0000	undef	0.0000
Muscle-skeleton	0.0030	0.0000	undef	0.0000
Kidneys	0.0038	0.0000	undef	0.0000
Pancreas	0.0150	0.0000	undef	0.0000
Penis	0.0024	0.0106	0.2237	4.4697
Prostate	0.0116	0.0142	0.8123	1.2311
Uterus	0.0036			
Breast hyperplasia	0.0093			
Small intestine	0.0030			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0118			
Sensory organs	0.0000			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.1472
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0408
Ovary-uterus	0.0274
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0234
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 49

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0186	0.0077	2.4246 0.4124
Bladder	0.0293	0.0087	3.3637 0.2973
Breast	0.0091	0.0234	0.3895 2.5671
Ovary	0.0091	0.0327	0.2791 3.5833
Endocrine tissue	0.0116	0.0143	0.8143 1.2281
Gastrointestinal	0.0110	0.0110	1.0063 0.9937
Brain	0.0112	0.0000	undef 0.0000
Hematopoietic	0.0199	0.0000	undef 0.0000
Skin	0.0149	0.0065	2.2954 0.4356
Hepatic	0.0392	0.0000	undef 0.0000
Heart	0.0122	0.0117	1.0447 0.9572
Testicles	0.0224	0.0071	3.1603 0.3164
Lungs	0.0097	0.0230	0.4200 2.3811
Stomach-esophagus	0.0188	0.0300	0.6281 1.5921
Muscle-skeleton	0.0119	0.0137	0.8683 1.1517
Kidneys	0.0076	0.0000	undef 0.0000
Pancreas	0.0150	0.0267	0.5615 1.7808
Penis	0.0238	0.0128	1.8644 0.5364
Prostate	0.0198	0.0000	undef 0.0000
Uterus	0.0182		
Breast hyperplasia	0.0125		
Small intestine	0.0178		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0252		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0092
Brain	0.0063
Hematopoietic	0.0157
Heart-blood vessels	0.0245
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0997
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0297
Endocrine tissue	0.0000
Fetal	0.0251
Gastrointestinal	0.0732
Hematopoietic	0.0114
Skin-muscle	0.0615
Testicles	0.0234
Lungs	0.0164
Nerves	0.0171
Prostate	0.0192
Sensory organs	0.0232

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Electronic Northern Blot for SEQ. ID. NO: 50

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0091	0.0000	undef 0.0000
Ovary	0.0000	0.0109	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0011	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lungs	0.0075	0.0000	undef 0.0000
Stomach-esophagus	0.0386	0.0000	undef 0.0000
Muscle-skeleton	0.0017	0.0120	0.1428 7.0051
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0019	0.0055	0.3428 2.9168
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0024	0.0043	0.5593 1.7879
Uterus	0.0033	0.0000	undef 0.0000
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Ovary-uterus	0.0091
Endocrine tissue	0.0000
Fetal	0.0227
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0000
Lungs	0.0000
Nerves	0.0030
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 51

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0077	1.2123 0.8249
	0.0133	0.0000	undef 0.0000
Bladder	0.0000	0.0078	0.0000 undef
Breast	0.0018	0.0000	undef 0.0000
Ovary	0.0097	0.0095	1.0178 0.9825
Endocrine tissue	0.0025	0.0099	0.2580 3.8754
Gastrointestinal	0.0084	0.0378	0.2218 4.5091
Brain	0.0099	0.0847	0.1175 8.5131
Hematopoietic	0.0099	0.0065	1.5303 0.6535
Skin	0.0011	0.0000	undef 0.0000
Hepatic	0.0061	0.0000	undef 0.0000
Heart	0.0100	0.0095	1.0534 0.9493
Testicles	0.0000	0.0000	undef undef
Lungs	0.0343	0.0060	5.7101 0.1751
Stomach-esophagus	0.0000	0.0137	0.0000 undef
Muscle-skeleton	0.0000	0.0110	0.0000 undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0071	0.0043	1.6779 0.5960
Penis	0.0033	0.0071	0.4642 2.1544
Prostate	0.0000		
Uterus	0.0062		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0118		
Sensory organs	0.0209		
White blood cells			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0062
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0160
Endocrine tissue	0.0735
Fetal	0.0140
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 53

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0051	0.0000 undef
Bladder	0.0213	0.0044	4.8926 0.2044
Breast	0.0091	0.0182	0.5008 1.9967
Ovary	0.0091	0.0191	0.4784 2.0902
Endocrine tissue	0.0019	0.0190	0.1018 9.8248
Gastrointestinal	0.0034	0.0066	0.5161 1.9377
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0106	0.0000	undef 0.0000
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0075	0.0095	0.7901 1.2657
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0034	0.0000	undef 0.0000
Muscle-skeleton	0.0059	0.0137	0.4342 2.3033
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0150	0.1066	0.1404 7.1232
Penis	0.0119	0.0064	1.8644 0.5364
Prostate	0.0182	0.0071	2.5529 0.3917
Uterus	0.0254		
Breast hyperplasia	0.0093		
Small intestine	0.0059		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0204
Lungs	0.0370
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0087
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0164
Nerves	0.0010
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 54

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0093	0.0077	1.2123 0.8249
Bladder	0.0200	0.0044	4.5868 0.2180
Breast	0.0152	0.0104	1.4608 0.6846
Ovary	0.0091	0.0054	1.6745 0.5972
Endocrine tissue	0.0039	0.0048	0.8143 1.2281
Gastrointestinal	0.0110	0.0033	3.3545 0.2981
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0149	0.0000	undef 0.0000
Skin	0.0198	0.0000	undef 0.0000
Hepatic	0.0064	0.0000	undef 0.0000
Heart	0.0122	0.0000	undef 0.0000
Testicles	0.0062	0.0071	0.8779 1.1391
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0051	0.0240	0.2141 4.6701
Muscle-skeleton	0.0178	0.0000	undef 0.0000
Kidneys	0.0019	0.0110	0.1714 5.8337
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0119	0.0043	2.7966 0.3576
Prostate	0.0050	0.0214	0.2321 4.3088
Uterus	0.0000		
Breast hyperplasia	0.0062		
Small intestine	0.0208		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0540		

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0123
Brain	0.0250
Hematopoietic	0.0275
Heart-blood vessels	0.0082
Lungs	0.0037
Kidneys	0.0185
Prostate	0.0000
Sensory organs	0.0558

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0000
Lungs	0.0082
Nerves	0.0040
Prostate	0.0064
Sensory organs	0.0310

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Electronic Northern Blot for SEQ. ID. NO: 56

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0000	undef	0.0000
Bladder	0.0227	0.0044	5.1984	0.1924
Breast	0.0000	0.0000	undef	undef
Ovary	0.0018	0.0000	undef	0.0000
Endocrine tissue	0.0058	0.0048	1.2214	0.8187
Gastrointestinal	0.0059	0.0011	5.4187	0.1845
Brain	0.0014	0.0000	undef	0.0000
Hematopoietic	0.0050	0.0000	undef	0.0000
Skin	0.0446	0.0000	undef	0.0000
Hepatic	0.0095	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0075	0.0071	1.0534	0.9493
Lungs	0.0097	0.0307	0.3150	3.1748
Stomach-esophagus	0.0120	0.0000	undef	0.0000
Muscle-skeleton	0.0208	0.0068	3.0391	0.3290
Kidneys	0.0038	0.0110	0.3428	2.9168
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0119	0.0106	1.1186	0.8939
Prostate	0.0017	0.0000	undef	0.0000
Uterus	0.0254			
Breast hyperplasia	0.0000			
Small intestine	0.0059			
Prostatic hyperplasia	0.0089			
Seminal vesicles	0.0000			
Sensory organs	0.0383			
White blood cells				

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0118
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0057
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0082
Nerves	0.0070
Prostate	0.0128
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 57

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0000	undef	0.0000
Breast	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

	FETUS % freq.
Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0000
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 58

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0107	0.0000	undef 0.0000
Breast	0.0213	0.0026	8.1803 0.1222
Ovary	0.0000	0.0054	0.0000 undef
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0212	0.0077	2.7647 0.3617
Brain	0.0000	0.0378	0.0000 undef
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0021	0.0000	undef 0.0000
Heart	0.0244	0.0000	undef 0.0000
Testicles	0.0087	0.0047	1.8435 0.5424
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0030	0.0068	0.4342 2.3033
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0060	0.0000	undef 0.0000
Penis	0.0000	0.0021	0.0000 undef
Prostate	0.0033	0.0142	0.2321 4.3088
Uterus	0.0036		
Breast hyperplasia	0.0031		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0111
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0047
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0050
Prostate	0.0000
Sensory organs	0.0155

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Electronic Northern Blot for SEQ. ID. NO: 59

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0133	0.0000	undef 0.0000
Breast	0.0000	0.0104	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0000	0.0000	undef undef
Gastrointestinal	0.0008	0.0011	0.7741 1.2918
Brain	0.0000	0.0000	undef undef
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0011	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0025	0.0000	undef 0.0000
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0038	0.0000	undef 0.0000
Penis	0.0000	0.0000	undef undef
Prostate	0.0071	0.0021	3.3559 0.2980
Uterus	0.0017	0.0000	undef 0.0000
Breast hyperplasia	0.0036		
Small intestine	0.0031		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0279

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0082
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles	0.0156
Lungs	0.0000
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 60

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0186	0.0051	3.6370 0.2750
Bladder	0.0160	0.0044	3.6695 0.2725
Breast	0.0061	0.0052	1.1686 0.8557
Ovary	0.0201	0.1634	0.1228 8.1438
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0305	0.0110	2.7868 0.3588
Brain	0.0014	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0244	0.0275	0.8864 1.1282
Heart	0.0000	0.0000	undef undef
Testicles	0.0050	0.0047	1.0534 0.9493
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0120	0.0060	1.9985 0.5004
Muscle-skeleton	0.0000	0.0205	0.0000 undef
Kidneys	0.0000	0.0110	0.0000 undef
Pancreas	0.0359	0.0000	undef 0.0000
Penis	0.0119	0.0149	0.7990 1.2515
Prostate	0.0099	0.0071	1.3925 0.7181
Uterus	0.0109		
Breast hyperplasia	0.0093		
Small intestine	0.0059		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0353		
Sensory organs	0.0000		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0092
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0046
Endocrine tissue	0.0490
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0114
Skin-muscle	0.0000
Testicles	0.0156
Lungs	0.0082
Nerves	0.0161
Prostate	0.0000
Sensory organs	0.0000

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	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0046	0.0051	0.9092	1.0998
	0.0306	0.0022	14.0663	0.0711
Bladder	0.0030	0.0078	0.3895	2.5671
Breast	0.0055	0.0027	2.0093	0.4977
Ovary	0.0058	0.0238	0.2443	4.0937
Endocrine tissue	0.0068	0.0022	3.0964	0.3230
Gastrointestinal	0.0014	0.0000	undef	0.0000
Brain	0.0199	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0065	0.0000	undef
Skin	0.0085	0.0000	undef	0.0000
Hepatic	0.0061	0.0000	undef	0.0000
Heart	0.0075	0.0047	1.5801	0.6329
Testicles	0.0000	0.0077	0.0000	undef
Lungs	0.0017	0.0060	0.2855	3.5025
Stomach-esophagus	0.0030	0.0068	0.4342	2.3033
Muscle-skeleton	0.0000	0.0000	undef	undef
Kidneys	0.0060	0.0000	undef	0.0000
Pancreas	0.0024	0.0043	0.5593	1.7879
Penis	0.0033	0.0000	undef	0.0000
Prostate	0.0145			
Uterus	0.0125			
Breast hyperplasia	0.0059			
Small intestine	0.0000			
Prostatic hyperplasia	0.0235			
Seminal vesicles	0.0000			
Sensory organs	0.0235			
White blood cells	0.0000			

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0063
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

Breast	0.0068
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0128
Sensory organs	0.0155

Electronic Northern Blot for SEQ. ID. NO: 62

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0120	0.0022	5.5042 0.1817
Breast	0.0030	0.0104	0.2922 3.4228
Ovary	0.0055	0.0027	2.0093 0.4977
Endocrine tissue	0.0058	0.0048	1.2214 0.8187
Gastrointestinal	0.0119	0.0131	0.9031 1.1073
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0065	0.0000 undef
Hepatic	0.0000	0.0137	0.0000 undef
Heart	0.0183	0.0000	undef 0.0000
Testicles	0.0037	0.0024	1.5801 0.6329
Lungs	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0017	0.0060	0.2855 3.5025
Muscle-skeleton	0.0030	0.0000	undef 0.0000
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0090	0.0000	undef 0.0000
Penis	0.0024	0.0085	0.2797 3.5758
Prostate	0.0083	0.0142	0.5802 1.7235
Uterus	0.0073		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0353		
White blood cells	0.0044		

	FETUS % freq.
Development	0.0307
Gastrointestinal	0.0123
Brain	0.0000
Hematopoietic	0.0079
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0052
Gastrointestinal	0.0000
Hematopoietic	0.0171
Skin-muscle	0.0097
Testicles	0.0078
Lungs	0.0246
Nerves	0.0271
Prostate	0.0192
Sensory organs	0.0000

000260 69994660

Electronic Northern Blot for SEQ. ID. NO: 63

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0204	1.1366 0.8799
	0.0267	0.0087	3.0579 0.3270
Bladder	0.0304	0.0130	2.3372 0.4279
Breast	0.0529	0.0735	0.7194 1.3901
Ovary	0.0174	0.0048	3.6642 0.2729
Endocrine tissue	0.0170	0.0208	0.8148 1.2272
Gastrointestinal	0.0070	0.0378	0.1848 5.4110
Brain	0.0199	0.0000	undef 0.0000
Hematopoietic	0.0198	0.0000	undef 0.0000
Skin	0.0180	0.0550	0.3276 3.0528
Hepatic	0.0122	0.0117	1.0447 0.9572
Heart	0.0249	0.0118	2.1069 0.4746
Testicles	0.0386	0.0153	2.5198 0.3968
Lungs	0.0120	0.0180	0.6662 1.5011
Stomach-esophagus	0.0089	0.0068	1.3025 0.7678
Muscle-skeleton	0.0170	0.0055	3.0855 0.3241
Kidneys	0.0509	0.0000	undef 0.0000
Pancreas	0.0357	0.0149	2.3971 0.4172
Penis	0.0297	0.0214	1.3925 0.7181
Prostate	0.0000		
Uterus	0.0093		
Breast hyperplasia	0.0178		
Small intestine	0.0267		
Prostatic hyperplasia	0.0118		
Seminal vesicles	0.0000		
Sensory organs			
White blood cells			

	FETUS % freq.
	0.0154
Development	0.0185
Gastrointestinal	0.0125
Brain	0.0000
Hematopoietic	0.0491
Heart-blood vessels	0.0037
Lungs	0.0432
Kidneys	0.0000
Prostate	0.0000
Sensory organs	

STANDARDIZED/SUBTRACTED LIBRARIES

	% frequency
	0.0272
Breast	0.0342
Ovary-uterus	0.0000
Endocrine tissue	0.0157
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0648
Skin-muscle	0.0312
Testicles	0.0246
Lungs	0.0151
Nerves	0.0192
Prostate	0.0697
Sensory organs	

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Electronic Northern Blot for SEQ. ID. NO: 64

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0102	2.2731 0.4399
Bladder	0.0240	0.0065	3.6695 0.2725
Breast	0.0213	0.0416	0.5113 1.9559
Ovary	0.0237	0.0027	8.7071 0.1148
Endocrine tissue	0.0213	0.0381	0.5598 1.7863
Gastrointestinal	0.0136	0.0099	1.3762 0.7266
Brain	0.0042	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0248	0.0129	1.9129 0.5228
Hepatic	0.0191	0.0137	1.3873 0.7208
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0112	0.0095	1.1851 0.8438
Lungs	0.0097	0.0000	undef 0.0000
Stomach-esophagus	0.0051	0.0060	0.8565 1.1675
Muscle-skeleton	0.0149	0.0205	0.7236 1.3820
Kidneys	0.0076	0.0055	1.3713 0.7292
Pancreas	0.0269	0.0267	1.0108 0.9893
Penis	0.0333	0.0170	1.9576 0.5108
Prostate	0.0099	0.0071	1.3925 0.7181
Uterus	0.0145		
Breast hyperplasia	0.0343		
Small intestine	0.0178		
Prostatic hyperplasia	0.0089		
Seminal vesicles	0.0000		
Sensory organs	0.0139		
White blood cells			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0039
Heart-blood vessels	0.0082
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0249
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0137
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0227
Testicles	0.0000
Lungs	0.0000
Nerves	0.0110
Prostate	0.0385
Sensory organs	0.0155

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Electronic Northern Blot for SEQ. ID. NO: 65

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0139	0.0026	5.4554	0.1833
	0.0093	0.0022	4.2811	0.2336
Bladder	0.0000	0.0130	0.0000	undef
Breast	0.0036	0.0082	0.4465	2.2395
Ovary	0.0000	0.0095	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0028	0.0000	undef	0.0000
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0085	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0012	0.0000	undef	0.0000
Testicles	0.0193	0.0000	undef	0.0000
Lungs	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0019	0.0000	undef	0.0000
Kidneys	0.0060	0.0000	undef	0.0000
Pancreas	0.0048	0.0000	undef	0.0000
Penis	0.0066	0.0214	0.3094	3.2316
Prostate	0.0109			
Uterus	0.0093			
Breast hyperplasia	0.0000			
Small intestine	0.0178			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0041
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0078
Lungs	0.0164
Nerves	0.0000
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 66

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0077	0.0000 undef
Bladder	0.0120	0.0022	5.5042 0.1817
Breast	0.0030	0.0052	0.5843 1.7114
Ovary	0.0000	0.0054	0.0000 undef
Endocrine tissue	0.0039	0.0000	undef 0.0000
Gastrointestinal	0.0008	0.0033	0.2580 3.8754
Brain	0.0070	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0053	0.0000	undef 0.0000
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0062	0.0071	0.8779 1.1391
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0019	0.0000	undef 0.0000
Penis	0.0030	0.0000	undef 0.0000
Prostate	0.0119	0.0000	undef 0.0000
Uterus	0.0033	0.0071	0.4642 2.1544
Breast hyperplasia	0.0036		
Small intestine	0.0000		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0061		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0236
Heart-blood vessels	0.0082
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0046
Endocrine tissue	0.0000
Fetal	0.0023
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0130
Testicles	0.0078
Lungs	0.0000
Nerves	0.0020
Prostate	0.0000
Sensory organs	0.0000

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 67

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0232	0.0051	4.5462 0.2200
Bladder	0.0506	0.0044	11.6200 0.0861
Breast	0.0000	0.0000	undef undef
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0019	0.0000	undef 0.0000
Gastrointestinal	0.0034	0.0000	undef 0.0000
Brain	0.0028	0.0378	0.0739 13.5274
Hematopoietic	0.0348	0.0000	undef 0.0000
Skin	0.0000	0.0000	undef undef
Hepatic	0.0254	0.0137	1.8498 0.5406
Heart	0.0000	0.0000	undef undef
Testicles	0.0025	0.0071	0.3511 2.8478
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0017	0.0240	0.0714 14.0102
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Penis	0.0024	0.0000	undef 0.0000
Prostate	0.0017	0.0000	undef 0.0000
Uterus	0.0872		
Breast hyperplasia	0.0093		
Small intestine	0.0030		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0044		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0157
Heart-blood vessels	0.0082
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0023
Endocrine tissue	0.0000
Fetal	0.0035
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0020
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 68

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0046	0.0077	0.6062 1.6497
Bladder	0.0253	0.0044	5.8100 0.1721
Breast	0.0152	0.0312	0.4869 2.0537
Ovary	0.0146	0.0163	0.8930 1.1198
Endocrine tissue	0.0078	0.0048	1.6285 0.6141
Gastrointestinal	0.0170	0.0110	1.5482 0.6459
Brain	0.0056	0.0378	0.1478 6.7637
Hematopoietic	0.0099	0.0000	undef 0.0000
Skin	0.0050	0.0065	0.7651 1.3069
Hepatic	0.0106	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0050	0.0118	0.4214 2.3732
Lungs	0.0000	0.0077	0.0000 undef
Stomach-esophagus	0.0017	0.0300	0.0571 17.5127
Muscle-skeleton	0.0297	0.0205	1.4472 0.6910
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0180	0.0000	undef 0.0000
Penis	0.0048	0.0085	0.5593 1.7879
Prostate	0.0198	0.0142	1.3925 0.7181
Uterus	0.0327		
Breast hyperplasia	0.0125		
Small intestine	0.0059		
Prostatic hyperplasia	0.0000		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0154
Gastrointestinal	0.0123
Brain	0.0063
Hematopoietic	0.0079
Heart-blood vessels	0.0123
Lungs	0.0259
Kidneys	0.0124
Prostate	0.0000
Sensory organs	0.0140

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0023
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0082
Nerves	0.0141
Prostate	0.0064
Sensory organs	0.0000

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Electronic Northern Blot for SEQ. ID. NO: 69

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
	0.0000	0.0000	undef	undef
Bladder	0.0120	0.0000	undef	0.0000
Breast	0.0030	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Gastrointestinal	0.0051	0.0033	1.5482	0.6459
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0011	0.0000	undef	0.0000
Heart	0.0000	0.0000	undef	undef
Testicles	0.0037	0.0024	1.5801	0.6329
Lungs	0.0000	0.0077	0.0000	undef
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0059	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0000	0.0000	undef	undef
Prostate	0.0000	0.0000	undef	undef
Uterus	0.0000	0.0000	undef	undef
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0000			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0000
Endocrine tissue	0.0000
Fetal	0.0105
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0100
Prostate	0.0000
Sensory organs	0.0077

000260" 69594960

Electronic Northern Blot for SEQ. ID. NO: 71

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
Bladder	0.0232	0.0051	4.5462 0.2200
Breast	0.0173	0.0044	3.9753 0.2516
Ovary	0.0091	0.0000	undef 0.0000
Endocrine tissue	0.0055	0.0163	0.3349 2.9861
Gastrointestinal	0.0039	0.0048	0.8143 1.2281
Brain	0.0034	0.0131	0.2580 3.8754
Hematopoietic	0.0028	0.0000	undef 0.0000
Skin	0.0050	0.0000	undef 0.0000
Hepatic	0.0000	0.0129	0.0000 undef
Heart	0.0053	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef undef
Lungs	0.0062	0.0047	1.3168 0.7594
Stomach-esophagus	0.0097	0.0077	1.2599 0.7937
Muscle-skeleton	0.0034	0.0000	undef 0.0000
Kidneys	0.0119	0.0000	undef 0.0000
Pancreas	0.0076	0.0166	0.4571 2.1876
Penis	0.0150	0.0000	undef 0.0000
Prostate	0.0071	0.0085	0.8390 1.1919
Uterus	0.0165	0.0000	undef 0.0000
Breast hyperplasia	0.0073		
Small intestine	0.0031		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0026		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0062
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0123
Lungs	0.0074
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Ovary-uterus	0.0091
Endocrine tissue	0.0000
Fetal	0.0064
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles	0.0156
Lungs	0.0246
Nerves	0.0040
Prostate	0.0000
Sensory organs	0.0155

000260" 69594650

Electronic Northern Blot for SEQ. ID. NO: 72

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0026	0.0000 undef
Bladder	0.0107	0.0000	undef 0.0000
Breast	0.0000	0.0026	0.0000 undef
Ovary	0.0000	0.0027	0.0000 undef
Endocrine tissue	0.0078	0.0000	undef 0.0000
Gastrointestinal	0.0017	0.0055	0.3096 3.2295
Brain	0.0028	0.0000	undef 0.0000
Hematopoietic	0.0050	0.0000	undef 0.0000
Skin	0.0000	0.0129	0.0000 undef
Hepatic	0.0042	0.0000	undef 0.0000
Heart	0.0000	0.0000	undef undef
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0153	0.0000 undef
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0089	0.0000	undef 0.0000
Kidneys	0.0019	0.0000	undef 0.0000
Pancreas	0.0030	0.0000	undef 0.0000
Penis	0.0095	0.0043	2.2373 0.4470
Prostate	0.0017	0.0071	0.2321 4.3088
Uterus	0.0000		
Breast hyperplasia	0.0000		
Small intestine	0.0000		
Prostatic hyperplasia	0.0059		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0009		

FETUS
% freq.

	0.0000
Development	0.0092
Gastrointestinal	0.0000
Brain	0.0039
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

	0.0068
Breast	0.0068
Ovary-uterus	0.0000
Endocrine tissue	0.0035
Fetal	0.0000
Gastrointestinal	0.0171
Hematopoietic	0.0097
Skin-muscle	0.0000
Testicles	0.0082
Lungs	0.0030
Nerves	0.0128
Prostate	0.0000
Sensory organs	

000260" 6954960

Electronic Northern Blot for SEQ. ID. NO: 74

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
Bladder	0.0000	0.0026	0.0000	undef
Breast	0.0093	0.0000	undef	0.0000
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0018	0.0000	undef	0.0000
Gastrointestinal	0.0000	0.0000	undef	undef
Brain	0.0000	0.0000	undef	undef
Hematopoietic	0.0000	0.0000	undef	undef
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0032	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lungs	0.0000	0.0024	0.0000	undef
Stomach-esophagus	0.0097	0.0000	undef	0.0000
Muscle-skeleton	0.0017	0.0000	undef	0.0000
Kidneys	0.0000	0.0000	undef	undef
Pancreas	0.0000	0.0000	undef	undef
Penis	0.0030	0.0000	undef	0.0000
Prostate	0.0024	0.0000	undef	0.0000
Uterus	0.0083	0.0000	undef	0.0000
Breast hyperplasia	0.0000			
Small intestine	0.0000			
Prostatic hyperplasia	0.0000			
Seminal vesicles	0.0089			
Sensory organs	0.0000			
White blood cells	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Ovary-uterus	0.0114
Endocrine tissue	0.0245
Fetal	0.0006
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0000

000260" 6254960

Electronic Northern Blot for SEQ. ID. NO: 76

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
	0.0000	0.0153	0.0000 undef
Bladder	0.0080	0.0000	undef 0.0000
Breast	0.0030	0.0078	0.3895 2.5671
Ovary	0.0036	0.0000	undef 0.0000
Endocrine tissue	0.0000	0.0190	0.0000 undef
Gastrointestinal	0.0017	0.0033	0.5161 1.9377
Brain	0.0056	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Skin	0.0000	0.0000	undef undef
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0117	0.0000 undef
Testicles	0.0012	0.0024	0.5267 1.8986
Lungs	0.0000	0.0000	undef undef
Stomach-esophagus	0.0069	0.0000	undef 0.0000
Muscle-skeleton	0.0000	0.0000	undef undef
Kidneys	0.0000	0.0000	undef undef
Pancreas	0.0000	0.0000	undef undef
Penis	0.0060	0.0000	undef 0.0000
Prostate	0.0024	0.0021	1.1186 0.8939
Uterus	0.0000	0.0000	undef undef
Breast hyperplasia	0.0000		
Small intestine	0.0031		
Prostatic hyperplasia	0.0030		
Seminal vesicles	0.0000		
Sensory organs	0.0000		
White blood cells	0.0035		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0031
Brain	0.0000
Hematopoietic	0.0000
Heart-blood vessels	0.0000
Lungs	0.0000
Kidneys	0.0062
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Ovary-uterus	0.0000
Endocrine tissue	0.0735
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles	0.0000
Lungs	0.0000
Nerves	0.0010
Prostate	0.0000
Sensory organs	0.0077

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Electronic Northern for	Seq. ID.	TUMOR	RATIOS
	NORMAL % freq.	% freq.	N/T T/N
B lymphoma	0.0100	0.0136	0.7358 1.3590
Bladder	0.0195	0.0164	1.1854 0.8436
Breast	0.0176	0.0042	4.1747 0.2395
Large intestine	0.0115	0.0142	0.8073 1.2386
Small intestine	0.0055	0.0213	0.2577 3.8812
Ovary	0.0030	0.0095	0.3111 3.2146
Endocrine tissue	0.0048	0.0089	0.5432 1.8409
Brain	0.0104	0.0120	0.8704 1.1489
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0030	0.0137	0.2215 4.5144
Testicles	0.0120	0.0118	1.0178 0.9825
Lung	0.0049	0.0055	0.8770 1.1402
Stomach-esophagus	0.0072	0.0128	0.5668 1.7644
Muscle-skeleton	0.0154	0.0111	1.3917 0.7186
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0017	0.0166	0.0997 10.0282
Prostate	0.0075	0.0104	0.7235 1.3821
T lymphoma	0.0076	0.0448	0.1691 5.9152
Uterus	0.0089	0.0138	0.6426 1.5563
White blood cells	0.0096	0.0000	undef 0.0000
Hematopoietic	0.0094		
Penis	0.0054		
Seminal vesicle	0.0141		
Sensory organs			

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

Breast	
Breast_t	
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0101
Gastrointestinal	0.0000
Hematopoietic	0.0029
Skin-muscle	0.0244
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0084
Lungs_t	0.0000
Nerves	0.0000
Kidney_t	0.0000
Ovary uterus	0.0000
Prostate_n	0.0020
Sensory organs	0.0000
White blood cells	0.0090
	0.0121
	0.0000
	0.0000

Electronic Northern for Seq. ID: 162

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0078	0.0000	undef 0.0000
Breast	0.0123	0.0042	2.9223 0.3422
Large intestine	0.0096	0.0028	3.3639 0.2973
Small intestine	0.0000	0.0000	undef undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0032	0.0195	0.1646 6.0749
Brain	0.0041	0.0040	1.0155 0.9848
Skin	0.0110	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0080	0.0000	undef undef
Lung	0.0039	0.0018	2.1049 0.4751
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0051	0.0037	1.3917 0.7186
Kidney	0.0067	0.0000	undef 0.0000
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0075	0.0026	2.8941 0.3455
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0059	0.0276	0.2142 4.6688
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0013		
Penis	0.0134		
Seminal vesicle	0.0070		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0017
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0040
Kidney t	0.0000
Ovary uterus	0.0180
Prostate n	0.0061
Sensory organs	0.0542
White blood cells	0.0000

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Electronic Northern for Seq. ID: 163

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0025	0.0000	undef	0.0000
Bladder	0.0000	0.0000	undef	undef
Breast	0.0097	0.0000	undef	0.0000
Large intestine	0.0038	0.0057	0.6728	1.4864
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0000	0.0035	0.0000	undef
Brain	0.0041	0.0030	1.3539	0.7386
Skin	0.0110	0.0000	undef	0.0000
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0061	0.0000	undef	0.0000
Testicles	0.0080	0.0000	undef	0.0000
Lung	0.0039	0.0037	1.0524	0.9502
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0103	0.0000	undef	0.0000
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0000	0.0000	undef	undef
Prostate	0.0028	0.0013	2.1706	0.4607
T lymphoma	0.0025	0.0075	0.3381	2.9576
Uterus	0.0030	0.0000	undef	0.0000
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0000
Adrenal gland	0.0507
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0680
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0029
Gastrointestinal	0.0122
Hematopoietic	0.0513
Skin-muscle	0.0130
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0121
Kidney t	0.0000
Ovary uterus	0.0023
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0044	0.0000	undef	0.0000
Large intestine	0.0000	0.0057	0.0000	undef
Small intestine	0.0082	0.0000	undef	0.0000
Ovary	0.0030	0.0000	undef	0.0000
Endocrine tissue	0.0080	0.0035	2.2634	0.4418
Brain	0.0168	0.0080	2.1034	0.4754
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0063	0.0000	undef
Heart	0.0051	0.0000	undef	0.0000
Testicles	0.0040	0.0059	0.6786	1.4737
Lung	0.0029	0.0092	0.3157	3.1673
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0037	0.9278	1.0778
Kidney	0.0045	0.0096	0.4642	2.1540
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0085	0.0091	0.9302	1.0750
T lymphoma	0.0000	0.0149	0.0000	undef
Uterus	0.0030	0.0000	undef	0.0000
White blood cells	0.0027	0.0000	undef	0.0000
Hematopoietic	0.0013			
Penis	0.0054			
Seminal vesicle				
Sensory organs				

- Development
- Gastrointestinal
- Brain
- Hematopoietic
- Skin
- Hepatic
- Heart-blood vessels
- Lung
- Adrenal gland
- Kidney
- Placenta
- Prostate
- Sensory organs

STANDARDIZED/SUBTRACTED LIBRARIES

Breast
Breast_t
Large Intestine_t
Ovary_n
Ovary_t
Endocrine tissue
Fetal
Gastrointestinal
Hematopoietic
Skin-muscle
Testicles_n
Testicles_t
Lungs_n
Lungs_t
Nerves
Kidney_t
Ovary Uterus
Prostate_n
Sensory organs
White blood cells

Electronic Northern for Seq. ID: 165

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0000	0.0000	undef	undef
Breast	0.0106	0.0028	3.7573	0.2662
Large intestine	0.0000	0.0028	0.0000	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0095	0.0000	undef
Endocrine tissue	0.0000	0.0000	undef	undef
Brain	0.0012	0.0010	1.1605	0.8617
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0010	0.0137	0.0738	13.5431
Testicles	0.0000	0.0000	undef	undef
Lung	0.0068	0.0018	3.6835	0.2715
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0034	0.0000	undef	0.0000
Kidney	0.0045	0.0000	undef	0.0000
Pancreas	0.0033	0.0000	undef	0.0000
Prostate	0.0019	0.0013	1.4470	0.6911
T lymphoma	0.0076	0.0000	undef	0.0000
Uterus	0.0030	0.0046	0.6426	1.5563
White blood cells	0.0021	0.0000	undef	0.0000
Hematopoietic	0.0000			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0139
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0245
Fetal	0.0070
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0065
Testicles_n	0.0209
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0080
Kidney t	0.0000
Ovary uterus	0.0090
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0232
	0.0000

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Electronic Northern for Seq. ID: 166

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0075	0.0000	undef 0.0000
Bladder	0.0078	0.0023	3.3190 0.3013
Breast	0.0202	0.0042	4.8009 0.2083
Large intestine	0.0000	0.0028	0.0000 undef
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0032	0.0106	0.3018 3.3136
Brain	0.0168	0.0020	8.4138 0.1189
Skin	0.0147	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0132	0.0137	0.9599 1.0418
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0175	0.0148	1.1840 0.8446
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0051	0.0000	undef 0.0000
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0000	undef 0.0000
Prostate	0.0094	0.0039	2.4117 0.4146
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0080		
Seminal vesicle	0.0268		
Sensory organs	0.0211		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0188
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0145
Adrenal gland	0.0000
Kidney	0.0247
Placenta	0.0182
Prostate	0.0249
Sensory organs	0.0502

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0195
Lungs_t	0.0000
Nerves	0.0231
Kidney t	0.0000
Ovary Uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0077
White blood cells	0.0000

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Electronic Northern for Seq. ID: 167

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0078	0.0000	undef	0.0000
Breast	0.0141	0.0000	undef	0.0000
Large intestine	0.0019	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0030	0.0024	1.2443	0.8036
Endocrine tissue	0.0016	0.0035	0.4527	2.2091
Brain	0.0017	0.0010	1.7408	0.5745
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0112	0.0275	0.4061	2.4624
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0019	0.0074	0.2631	3.8007
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0086	0.0000	undef	0.0000
Kidney	0.0022	0.0000	undef	0.0000
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0019	0.0000	undef	0.0000
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0044	0.0092	0.4819	2.0750
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0080			
Seminal vesicle	0.0070			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0191
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0065
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 168

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0132	0.0000	undef 0.0000
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0000	0.0000	undef undef
Endocrine tissue	0.0016	0.0000	undef 0.0000
Brain	0.0006	0.0030	0.1934 5.1701
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0000	0.0000	undef undef
Lung	0.0000	0.0000	undef 0.0000
Stomach-esophagus	0.0039	0.0000	undef undef
Muscle-skeleton	0.0000	0.0000	undef 0.0000
Kidney	0.0034	0.0037	0.9278 1.0778
Pancreas	0.0045	0.0000	undef 0.0000
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0047	0.0039	1.2059 0.8293
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0044	0.0000	undef 0.0000
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0013		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0051
Ovary_t	0.0000
Endocrine tissue	0.0023
Fetal	0.0122
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0000
Ovary uterus	0.0068
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 169

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0039	0.0023	1.6595	0.6026
Breast	0.0106	0.0028	3.7573	0.2662
Large intestine	0.0096	0.0000	undef	0.0000
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0000	undef	undef
Endocrine tissue	0.0032	0.0018	1.8107	0.5523
Brain	0.0012	0.0030	0.3868	2.5851
Skin	0.0000	0.0000	undef	undef
Hepatic	0.0046	0.0000	undef	0.0000
Heart	0.0020	0.0000	undef	0.0000
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0039	0.0000	undef	0.0000
Stomach-esophagus	0.0072	0.0000	undef	0.0000
Muscle-skeleton	0.0069	0.0037	1.8555	0.5389
Kidney	0.0112	0.0048	2.3212	0.4308
Pancreas	0.0033	0.0000	undef	0.0000
Prostate	0.0009	0.0000	undef	0.0000
T lymphoma	0.0000	0.0000	undef	undef
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0136
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0490
Fetal	0.0197
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0020
Ovary uterus	0.0000
Prostate n	0.0045
Sensory organs	0.0121
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 170

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0117	0.0141	0.8297 1.2052
Breast	0.0194	0.0056	3.4442 0.2903
Large intestine	0.0057	0.0000	undef 0.0000
Small intestine	0.0055	0.0000	undef 0.0000
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0032	0.0018	1.8107 0.5523
Brain	0.0069	0.0140	0.4974 2.0106
Skin	0.0367	0.0000	undef 0.0000
Hepatic	0.0046	0.0000	undef 0.0000
Heart	0.0101	0.0000	undef 0.0000
Testicles	0.0000	0.0000	undef 0.0000
Lung	0.0049	0.0055	0.8770 1.1402
Stomach-esophagus	0.0000	0.0000	undef undef
Muscle-skeleton	0.0103	0.0000	undef undef
Kidney	0.0134	0.0048	2.7855 0.3590
Pancreas	0.0017	0.0055	0.2992 3.3427
Prostate	0.0028	0.0013	2.1706 0.4607
T lymphoma	0.0000	0.0000	undef undef
Uterus	0.0030	0.0000	undef 0.0000
White blood cells	0.0199	0.0000	undef 0.0000
Hematopoietic	0.0040	0.0000	undef 0.0000
Penis	0.0000		
Seminal vesicle	0.0141		
Sensory organs	0.0118		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0000
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0121
Prostate	0.0000
Sensory organs	0.0251

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0000
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0051
Endocrine tissue	0.0000
Fetal	0.0000
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0065
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0050
Ovary uterus	0.0000
Prostate n	0.0023
Sensory organs	0.0000
White blood cells	0.0000

Electronic Northern for Seq. ID: 171

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0250	0.0000	undef	0.0000
Bladder	0.0546	0.0188	2.9041	0.3443
Breast	0.0387	0.0056	6.8883	0.1452
Large intestine	0.0287	0.0000	undef	0.0000
Small intestine	0.0302	0.0107	2.8342	0.3528
Ovary	0.0237	0.0024	9.9547	0.1005
Endocrine tissue	0.0112	0.0106	1.0563	0.9467
Brain	0.0093	0.0060	1.5474	0.6463
Skin	0.0220	0.0000	undef	0.0000
Hepatic	0.0046	0.0063	0.7324	1.3653
Heart	0.0304	0.0000	undef	0.0000
Testicles	0.0161	0.0000	undef	0.0000
Lung	0.0175	0.0092	1.8944	0.5279
Stomach-esophagus	0.0145	0.0064	2.2671	0.4411
Muscle-skeleton	0.0188	0.0074	2.5514	0.3919
Kidney	0.0134	0.0048	2.7855	0.3590
Pancreas	0.0017	0.0000	undef	0.0000
Prostate	0.0254	0.0221	1.1491	0.8702
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0414	0.0184	2.2490	0.4446
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0160			
Penis	0.0724			
Seminal vesicle	0.0352			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0197
Skin	0.0000
Hepatic	0.0260
Heart-blood vessels	0.0036
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0309
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0952
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0127
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0084
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary Uterus	0.0000
Prostate n	0.0203
Sensory organs	0.0243
White blood cells	0.0000
	0.0000

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Electronic Northern for Seq. ID: 172

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0000	0.0000	undef undef
Bladder	0.0039	0.0023	1.6595 0.6026
Breast	0.0176	0.0042	4.1747 0.2395
Large intestine	0.0038	0.0028	1.3456 0.7432
Small intestine	0.0137	0.0107	1.2883 0.7762
Ovary	0.0000	0.0048	0.0000 undef
Endocrine tissue	0.0000	0.0000	undef undef
Brain	0.0006	0.0090	0.0645 15.5103
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0000	undef undef
Heart	0.0000	0.0000	undef undef
Testicles	0.0081	0.0000	undef 0.0000
Lung	0.0000	0.0000	undef undef
Stomach-esophagus	0.0029	0.0037	0.7893 1.2669
Muscle-skeleton	0.0072	0.0192	0.3778 2.6466
Kidney	0.0154	0.0037	4.1750 0.2395
Pancreas	0.0022	0.0048	0.4642 2.1540
Prostate	0.0000	0.0000	undef undef
T lymphoma	0.0132	0.0052	2.5323 0.3949
Uterus	0.0000	0.0000	undef undef
White blood cells	0.0030	0.0322	0.0918 10.8939
Hematopoietic	0.0000	0.0000	undef undef
Penis	0.0000	0.0000	undef undef
Seminal vesicle	0.0000		
Sensory organs	0.0080		

0.0141
0.0118
FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0181
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0012
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0020
Kidney t	0.0000
Ovary uterus	0.0000
Prostate n	0.0068
Sensory organs	0.0121
White blood cells	0.0000

0.0000

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Electronic Northern for Seq. ID: 173

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0050	0.0000	undef	0.0000
Bladder	0.0000	0.0047	0.0000	undef
Breast	0.0053	0.0014	3.7573	0.2662
Large intestine	0.0000	0.0000	undef	undef
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0089	0.0000	undef	0.0000
Endocrine tissue	0.0000	0.0089	0.0000	undef
Brain	0.0006	0.0030	0.1934	5.1701
Skin	0.0037	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0000	0.0000	undef	undef
Testicles	0.0000	0.0000	undef	undef
Lung	0.0000	0.0000	undef	undef
Stomach-esophagus	0.0088	0.0000	undef	0.0000
Muscle-skeleton	0.0217	0.0000	undef	0.0000
Kidney	0.0034	0.0074	0.4639	2.1557
Pancreas	0.0022	0.0000	undef	0.0000
Prostate	0.0017	0.0055	0.2992	3.3427
T lymphoma	0.0047	0.0039	1.2059	0.8293
Uterus	0.0000	0.0000	undef	undef
White blood cells	0.0030	0.0000	undef	0.0000
Hematopoietic	0.0000	0.0000	undef	undef
Penis	0.0027	0.0000	undef	undef
Seminal vesicle	0.0054			
Sensory organs	0.0000			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0063
Hematopoietic	0.0079
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0254
Kidney	0.0124
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0204
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0203
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0042
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0030
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0061
White blood cells	0.0000

0.0000

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Electronic Northern for Seq. ID: 174

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0100	0.0136	0.7358	1.3590
Bladder	0.0078	0.0070	1.1063	0.9039
Breast	0.0114	0.0028	4.0704	0.2457
Large intestine	0.0077	0.0057	1.3456	0.7432
Small intestine	0.0082	0.0213	0.3865	2.5875
Ovary	0.0000	0.0072	0.0000	undef
Endocrine tissue	0.0032	0.0000	undef	0.0000
Brain	0.0017	0.0090	0.1934	5.1701
Skin	0.0073	0.0394	0.1862	5.3697
Hepatic	0.0093	0.0063	1.4649	0.6826
Heart	0.0010	0.0000	undef	0.0000
Testicles	0.0000	0.0000	undef	undef
Lung	0.0107	0.0092	1.1577	0.8638
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0377	0.0037	10.2055	0.0980
Kidney	0.0000	0.0096	0.0000	undef
Pancreas	0.0000	0.0110	0.0000	undef
Prostate	0.0028	0.0026	1.0853	0.9214
T lymphoma	0.0051	0.0075	0.6762	1.4788
Uterus	0.0030	0.0046	0.6426	1.5563
White blood cells	0.0164	0.0304	0.5410	1.8483
Hematopoietic	0.0094			
Penis	0.0027			
Seminal vesicle	0.0000			
Sensory organs	0.0118			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0028
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0000
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
0.0000 % frequency

Breast	0.0000
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0152
Ovary_t	0.0735
Endocrine tissue	0.0151
Fetal	0.0366
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0010
Kidney t	0.0000
Ovary uterus	0.0225
Prostate n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 175

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0312	0.0047	6.6380	0.1506
Breast	0.0158	0.0056	2.8179	0.3549
Large intestine	0.0038	0.0000	undef	0.0000
Small intestine	0.0082	0.0213	0.3865	2.5875
Ovary	0.0059	0.0024	2.4887	0.4018
Endocrine tissue	0.0177	0.1277	0.1383	7.2297
Brain	0.0220	0.0100	2.2050	0.4535
Skin	0.0073	0.0000	undef	0.0000
Hepatic	0.0000	0.0000	undef	undef
Heart	0.0244	0.0275	0.8861	1.1286
Testicles	0.0040	0.0000	undef	0.0000
Lung	0.0078	0.0037	2.1049	0.4751
Stomach-esophagus	0.0000	0.0000	undef	undef
Muscle-skeleton	0.0120	0.0000	undef	0.0000
Kidney	0.0000	0.0145	0.0000	undef
Pancreas	0.0000	0.0110	0.0000	undef
Prostate	0.0075	0.0078	0.9647	1.0366
T lymphoma	0.0025	0.0000	undef	0.0000
Uterus	0.0103	0.0046	2.2490	0.4446
White blood cells	0.0000	0.0000	undef	undef
Hematopoietic	0.0013			
Penis	0.0375			
Seminal vesicle	0.0141			
Sensory organs	0.0353			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0071
Lung	0.0000
Adrenal gland	0.0254
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0126

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0490
Fetal	0.0035
Gastrointestinal	0.0244
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0125
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0161
Kidney t	0.0000
Ovary uterus	0.0045
Prostate n	0.0000
Sensory organs	0.0000
White blood cells	0.0000

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Electronic Northern for Seq. ID: 176

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0025	0.0000	undef 0.0000
Bladder	0.0078	0.0047	1.6595 0.6026
Breast	0.0202	0.0028	7.2014 0.1389
Large intestine	0.0057	0.0142	0.4037 2.4773
Small intestine	0.0110	0.0000	undef 0.0000
Ovary	0.0030	0.0072	0.4148 2.4109
Endocrine tissue	0.0064	0.0035	1.8107 0.5523
Brain	0.0058	0.0020	2.9013 0.3447
Skin	0.0147	0.0000	undef 0.0000
Hepatic	0.0000	0.0063	0.0000 undef
Heart	0.0081	0.0000	undef 0.0000
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0068	0.0055	1.2278 0.8144
Stomach-esophagus	0.0000	0.0064	0.0000 undef
Muscle-skeleton	0.0017	0.0037	0.4639 2.1557
Kidney	0.0022	0.0048	0.4642 2.1540
Pancreas	0.0000	0.0000	undef undef
Prostate	0.0028	0.0026	1.0853 0.9214
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0030	0.0000	undef 0.0000
White blood cells	0.0000	0.0000	undef undef
Hematopoietic	0.0027		
Penis	0.0054		
Seminal vesicle	0.0000		
Sensory organs	0.0235		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0056
Brain	0.0063
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0072
Adrenal gland	0.0000
Kidney	0.0000
Placenta	0.0061
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast_t	0.0000
Large intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0058
Gastrointestinal	0.0000
Hematopoietic	0.0000
Skin-muscle	0.0000
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0000
Lungs_t	0.0000
Nerves	0.0020
Kidney_t	0.0000
Ovary uterus	0.0135
Prostate_n	0.0061
Sensory organs	0.0155
White blood cells	0.0000

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Electronic Northern for Seq. ID: 177

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N
B lymphoma	0.0050	0.0000	undef 0.0000
Bladder	0.0000	0.0023	0.0000 undef
Breast	0.0079	0.0014	5.6359 0.1774
Large intestine	0.0096	0.0000	undef 0.0000
Small intestine	0.0000	0.0107	0.0000 undef
Ovary	0.0000	0.0024	0.0000 undef
Endocrine tissue	0.0016	0.0089	0.1811 5.5227
Brain	0.0023	0.0050	0.4642 2.1542
Skin	0.0073	0.0000	undef 0.0000
Hepatic	0.0000	0.0127	0.0000 undef
Heart	0.0030	0.0137	0.2215 4.5144
Testicles	0.0040	0.0000	undef 0.0000
Lung	0.0019	0.0018	1.0524 0.9502
Stomach-esophagus	0.0000	0.0128	0.0000 undef
Muscle-skeleton	0.0017	0.0000	undef 0.0000
Kidney	0.0045	0.0000	undef 0.0000
Pancreas	0.0033	0.0000	undef 0.0000
Prostate	0.0066	0.0026	2.5323 0.3949
T lymphoma	0.0025	0.0000	undef 0.0000
Uterus	0.0015	0.0046	0.3213 3.1125
White blood cells	0.0034	0.0000	undef 0.0000
Hematopoietic	0.0040		
Penis	0.0080		
Seminal vesicle	0.0000		
Sensory organs	0.0000		

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0083
Brain	0.0000
Hematopoietic	0.0039
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0000
Lung	0.0036
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0000
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0068
Breast t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0000
Endocrine tissue	0.0000
Fetal	0.0041
Gastrointestinal	0.0122
Hematopoietic	0.0000
Skin-muscle	0.0097
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0098
Lungs_t	0.0000
Nerves	0.0000
Kidney t	0.0040
Ovary uterus	0.0000
Prostate n	0.0090
Sensory organs	0.0061
White blood cells	0.0000

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Electronic Northern for Seq. ID: 178

	NORMAL % freq.	TUMOR % freq.	RATIOS N/T T/N	
B lymphoma	0.0000	0.0000	undef	undef
Bladder	0.0078	0.0258	0.3017	3.3143
Breast	0.0070	0.0042	1.6699	0.5988
Large intestine	0.0172	0.0114	1.5138	0.6606
Small intestine	0.0000	0.0000	undef	undef
Ovary	0.0000	0.0167	0.0000	undef
Endocrine tissue	0.0080	0.0018	4.5268	0.2209
Brain	0.0041	0.0080	0.5077	1.9696
Skin	0.0147	0.0000	undef	0.0000
Hepatic	0.0046	0.0190	0.2441	4.0959
Heart	0.0112	0.0137	0.8122	1.2312
Testicles	0.0000	0.0000	undef	undef
Lung	0.0214	0.0240	0.8905	1.1229
Stomach-esophagus	0.0362	0.0192	1.8892	0.5293
Muscle-skeleton	0.0137	0.0074	1.8555	0.5389
Kidney	0.0000	0.0048	0.0000	undef
Pancreas	0.0116	0.0166	0.6980	1.4326
Prostate	0.0104	0.0182	0.5685	1.7591
T lymphoma	0.0051	0.0000	undef	0.0000
Uterus	0.0044	0.0046	0.9638	1.0375
White blood cells	0.0055	0.0000	undef	0.0000
Hematopoietic	0.0053			
Penis	0.0107			
Seminal vesicle	0.0000			
Sensory organs	0.0235			

FETUS
% freq.

Development	0.0000
Gastrointestinal	0.0111
Brain	0.0000
Hematopoietic	0.0000
Skin	0.0000
Hepatic	0.0000
Heart-blood vessels	0.0036
Lung	0.0108
Adrenal gland	0.0000
Kidney	0.0062
Placenta	0.0242
Prostate	0.0000
Sensory organs	0.0000

STANDARDIZED/SUBTRACTED LIBRARIES
% frequency

Breast	0.0340
Breast_t	0.0000
Large Intestine_t	0.0000
Ovary_n	0.0000
Ovary_t	0.0101
Endocrine tissue	0.0000
Fetal	0.0081
Gastrointestinal	0.0366
Hematopoietic	0.0000
Skin-muscle	0.0194
Testicles_n	0.0000
Testicles_t	0.0000
Lungs_n	0.0293
Lungs_t	0.0000
Nerves	0.0030
Kidney_t	0.0000
Ovary uterus	0.0045
Prostate_n	0.0061
Sensory organs	0.0000
White blood cells	0.0000

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2.2. Fisher Test

In order to decide whether a partial sequence S of a gene occurs significantly more often or less often in a library for normal tissue than in a library for degenerated tissue, Fisher's exact test, a standard statistical process, is carried out (Hays, W. L., (1991) Statistics, Harcourt Brace College Publishers, Fort Worth).

The null hypothesis reads: The two libraries cannot be distinguished with respect to the frequency of sequences homologous to S . If the null hypothesis can be rejected with high enough certainty, the gene belonging to S is accepted as an advantageous candidate for a cancer gene, and in the next step an attempt is made to achieve lengthening of its sequence.

Example 3

Automatic lengthening of the partial sequence

Automatic lengthening of partial sequence S is completed in three steps:

1. Determination of all sequences homologous to S from the total set of available sequences using BLAST
2. Assembling these sequences by means of the standard program GAP4 (Bonfield, J. K.; Smith, K. F. and Staden, R. (1995), Nucleic Acids Research 23 4992-4999) (contig formation).
3. Computation of a consensus sequence C from the assembled sequences.

The consensus sequence C will generally be longer than initial sequence S . Its electronic Northern Blot will

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accordingly deviate from that for S. A repeated Fisher test decides whether the alternative hypothesis of deviation from a uniform expression in the two libraries can be maintained. If this is the case, an attempt is made to lengthen C in the same way as S. This iteration is continued with consensus sequences C_i (i : iteration index) obtained in each case until the alternative hypothesis is rejected (if H_0 Exit; truncation criterion I) or until automatic lengthening is no longer possible (while $C_i > C_{i-1}$; truncation criterion II).

In the case of truncation criterion II, with the consensus sequence present after the last iteration, a complete or roughly complete sequence of a gene which can be related to cancer with high statistical certainty is acquired.

Analogously to the above-described examples, it was possible to find from breast tissue the nucleic acid sequences described in Table I.

Furthermore, for the individual nucleic acid sequences, it was possible to determine the peptide sequences (ORFs) that are listed in Table II, in which no peptide can be assigned to a few nucleic acid sequences and more than one peptide can be assigned to some nucleic acid sequences. As already mentioned above, both the determined nucleic acid sequences and the peptide sequences assigned to the nucleic acid sequences are the subject of this invention.

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Mapping of nucleic acid sequences on the human genome

In addition to mapping of genes on the human chromosome set by various experimental methods, it is possible to determine the location of genes on this by biocomputer methods. To do this, the known program e-PCR was used (Schuler GD (1998) Electronic PCR: Bridging the gap between genome mapping and genome sequencing. Trends Biotechnol 16: 456-459, Schuler GD (1997). Sequence mapping by electronic PCR. Genome Res. 7: 541-550). The database used here no longer corresponds to the one cited in the literature, but is a further development which includes data from the public database RHdb (<http://www.ebi.ac.uk/RHdb/-index.html>). Analogously to the mapping by the hybrid panels,

the results were evaluated with the above-mentioned software and the software of the Whitehead Institute (<http://carbon.wi.mit.edu:8000/cgi-bin/contig/rhmapper.pl>).

Example 5

Obtaining genomic DNA sequences (BAC clones)

The genomic sequences that correspond to the differential cDNAs were isolated from commercial BAC libraries. BAC libraries of the Genome Systems Company, St. Louis, MO, which were produced from human lymphocytes, were used (<http://www.genomesystems.com>) and those of the Research Genetics Company, which were described as follows, were used: Shizuya, H.; B. Birren, U-J. Kim, V. Mancino, T. Slepak, Y. Tachiiri, M. Simon (1992) Proc. Natl. Acad. Sci., USA 89: 8794-8797; <http://www.tree.caltech.edu/>. From these libraries, the BAC clones with the procedure of "down-to-the-well" were isolated. In this procedure, a library consisting of BAC clones (the library covers roughly 3x the human genome) is combined in various groups (pools). This takes place in such a way that after the execution of a gene-specific PCR in the various pools, a definite clone assignment is possible. This address together with the name of the library which is being used unequivocally fixes the clones and thus the DNA sequence of these clones.

The following examples explain the successful isolation of the genomic BAC clones without limiting them thereto.

The libraries of genome systems used were CITB B and CITB C. Clones from the library of Research Genetics are underlined.

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Normal Breast

Seq. ID No.	Identified BACs				
4	174/F/16				
12	388/D/5	393/M/24	494/B/3	502/B/23	
13	203/A/1	233/B/22	392/L/10	311/J/7	
15	248/C/14	266/E/16	528/D/3	266/E/17	506/P/12
19	113/G/13	191/B/19	202/O/3	250/O/19	
21	137/H/19	231/I/10			
22	165/N/5	208/D/7			
26	6/L/15	11/I/17	117/E/15		
28	501/L/21	367/D/6			
31	369/H/21	429/I/13			
34	108/M/13				
37	289/C/11				
42	59/A/20				
43	325/J/11	448/O/2	563/F/18		
57	4/G/9				
58	229/O/21	233/F/12			
59	97/P/23	109/A/1	125/H/9		
60	503/P/21				
61	3/P/21	188/B/9			
63	176/A/22				
69	425/E/10				
71	178/I/19	242/B/6	242/B/11		

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TABLE I

Col. 1 - Ser. No.
 Col. 2 - Expression
 Col. 3 - Function
 Col. 4 - Modules
 Col. 5 - Chromosomal localization
 Col. 6 - Next marker
 Col. 7 - EST length (bp)
 Col. 8 - Length of the applied sequence (bp)

[Key:]

unbekannt = unknown

zwischen...und = between...and

Domäne = domain

"PH"-Domäne und "Spectrin"-Domäne = "PH" domain and "spectrin" domain

"crystallin"-Domäne und "HSP20"-Domäne = "crystalline" domain and "HSP20" domain

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"crystallin"-Domäne und "HSP20"-Domäne = "crystalline" domain and "HSP20" domain

TABLE I

Ser. No.	Expression	Function
1	Elevated in normal breast tissue	A new human pre-mRNA splice factor, which is part of a gene family with a TPR (tetratricopeptide repeats) motif.
2	Elevated in normal breast tissue	Unknown
3	Elevated in normal breast tissue	The human homolog of perilipin A from the rat.
4	Elevated in normal breast tissue	Unknown
5	Elevated in normal breast tissue	Unknown
10	Elevated in normal breast tissue	A human ortholog of fsp-27 (fat-specific protein 27) of the mouse.
11	Elevated in normal breast tissue	Unknown
12	Elevated in normal breast tissue	Unknown

[Key:]

unbekannt = unknown

zwischen...und = between...and

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
1	im normalen Brustgewebe erhöht	Ein neuer humaner Prä-mRNA Spleiß-Faktor, der zur einer Genfamilie mit TPR (Tetratricopeptid repeats)-Motiv gehört.	"TPR"-Region	unbekannt	unbekannt	205	2031
2	im normalen Brustgewebe erhöht	unbekannt		3q29	zwischen D3S1265 und D3S1311	248	1081
3	im normalen Brustgewebe erhöht	Das humane Homolog des Perilipin A aus Ratte.		15q26.1-qter	SHGC-6068; zwischen WI-7918 und SHGC-14718	247	1318
4	im normalen Brustgewebe erhöht	unbekannt		Xq24	SHGC-14021 alias DXS9764	256	731
5	im normalen Brustgewebe erhöht	unbekannt		15q26.1-qter	D15S120-15qter	237	2719
10	im normalen Brustgewebe erhöht	Ein humanes Ortholog des fsp-27 (Fett-spezifisches Protein 27) der Maus.		3p24.3-p25.1	zwischen D3S1597 und D3S1263	310	1107
11	im normalen Brustgewebe erhöht	unbekannt		17q22-q23.2	SHGC-32689; zwischen D17S787 und D17S792	239	1062
12	im normalen Brustgewebe erhöht	unbekannt		2q34	SHGC-3316; zwischen D2S315 und D2S2237	241	1471

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Ser. No.	Expression	Function
13	Elevated in normal breast tissue	The human LOT1 (Lost on Transformation 1).
14	Elevated in normal breast tissue	The human SGN3 (subunit 3 of a JAB1-containing signalosome).
15	Elevated in normal breast tissue	A new zinc finger protein of LIM type.
16	Elevated in normal breast tissue	The human nuclear factor I-B2 (NFIB2).
18	Elevated in normal breast tissue	The human dermatopontine.
19	Elevated in normal breast tissue	Unknown
21	Elevated in normal breast tissue	Unknown

[Key:]

Domäne = domain

unbekannt = unknown

zwischen...und = between...and

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
13	im normalen Brustgewebe erhöht	Das humane LOT1 (Lost On Transformation 1).	"ZINC_FINGER_C2H2"-Domäne	6q23.3-q24.3	zwischen D6S308 und D6S978	214	2738
14	im normalen Brustgewebe erhöht	Das humane SGN3 (die Untereinheit 3 eines JAB1 enthaltenden Signalosoms).	"PCI_DOMAIN"	17p12-q11.2	sts-W80395; zwischen D17S922 und D17S798	225	1710
15	im normalen Brustgewebe erhöht	Ein neues Zinkfinger-Protein des LIM-Typs.	"LIM"-Domäne	4p14	SHGC4-435; zwischen SHGC4-259 und SHGC-33782	228	3159
16	im normalen Brustgewebe erhöht	Der humane nukleäre Faktor I-B2 (NFIB2).		unbekannt	unbekannt	249	1680
18	im normalen Brustgewebe erhöht	Das humane Dermato pontin.		1q12-q23	unbekannt	188	1722
19	im normalen Brustgewebe erhöht	unbekannt		1p22.1-p22.2	SHGC-34523	287	1612
21	im normalen Brustgewebe erhöht	unbekannt		11q14.1	SHGC-32865; zwischen SHGC-3911 und SHGC-36303	248	1304

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Ser. No.	Expression	Function
22	Elevated in normal breast tissue	This sequence is related to heavy chain H3 of the human inter-alpha-trypsin inhibitor. The latter possibly plays a role in the stabilization of the extracellular matrix.
23	Elevated in normal breast tissue	Unknown
24	Elevated in normal breast tissue	Unknown
25	Elevated in normal breast tissue	Unknown
26	Elevated in normal breast tissue	The pi-subunit of the human GABA-A receptor.
28	Elevated in normal breast tissue	This sequence is possibly the ortholog of the neural membrane protein 35 (NMP35) of the rat.

[Key:]

Domäne = domain

zwischen...und = between...and

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
22	im normalen Brustgewebe erhöht	Diese Sequenz ist verwandt mit der schweren Kette H3 des humanen Inter-alpha-Trypsin Inhibitors. Dieser spielt möglicherweise eine Rolle bei der Stabilisierung der extrazellulären Matrix.		10p15.1-p15.3	SHGC-16603; zwischen SHGC-16603 und SHGC-33903	288	1533
23	im normalen Brustgewebe erhöht	unbekannt		11q14.2-q14.3	zwischen D11S1354 und D11S931	204	1304
24	im normalen Brustgewebe erhöht	unbekannt		10p15.1-p15.3	zwischen D10S591 und D10S189	291	2403
25	im normalen Brustgewebe erhöht	unbekannt		2q35	AFM249wg9; zwischen CHLC.GATA29E02 und WI-7744	286	2517
26	im normalen Brustgewebe erhöht	Die pi-Untereinheit des humanen GABA-A Rezeptors.	"neur_chan"-Domäne	5q34	AFM304xd5; zwischen AFM080xh11 und SHGC-5539	268	1668
28	im normalen Brustgewebe erhöht	Diese Sequenz ist möglicherweise das Ortholog des Neuralen Membran Protein 35 (NMP35) der Ratte.	"UPF0005"-Domäne	2q35	SHGC-35278; zwischen D2S164 und D2S163	244	1768

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Ser. No.	Expression	Function
29	Elevated in normal breast tissue	The human β -spectrin.
30	Elevated in normal breast tissue	Unknown
31	Elevated in normal breast tissue	This sequence probably represents the human ortholog of the "SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2)" of the hamster.
32	Elevated in normal breast tissue	The human protein kinase A anchor-protein; it binds the regulatory subunit (RII) of the protein-kinase A.
33	Elevated in normal breast tissue	The human Mi-2 autoantigen, in this connection it is presumably a helicase, which activates the transcription.
34	Elevated in normal breast tissue	Unknown
35	Elevated in normal breast tissue	The human "obese protein" (ob).

lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
29	im normalen Brustgewebe erhöht	Das humane β -Spectrin.	"PH"-Domäne und "Spectrin"-Domäne	2p16.1-16.3	zwischen D2S123 und D2S378	247	3479
30	im normalen Brustgewebe erhöht	unbekannt		7p21.2-p21.3	SHGC-35668; zwischen D7S714 und D7S2564	88	933
31	im normalen Brustgewebe erhöht	Diese Sequenz stellt wahrscheinlich das humane Ortholog des "SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2)" des Hamsters dar.	"LIM"-Domäne	12p11.21-q13.11	zwischen D12S1648 und D12S1620	269	2783
32	im normalen Brustgewebe erhöht	Das humane Protein Kinase A Anker-Protein; es bindet die regulatorische Untereinheit (RII) der Protein-Kinase A.	"KH"-Domäne und "TUDOR"-Domäne	17q22	zwischen D17S790 und D17S794	265	3411
33	im normalen Brustgewebe erhöht	Das humane Mi-2 Autoantigen, es handelt sich hierbei vermutlich um eine Helicase, die die Transkription aktiviert.		12p12.3-p13.33	zwischen D12S93 und D12S77	244	1393
34	im normalen Brustgewebe erhöht	unbekannt		10q25.1	SHGC-14061; zwischen ATC3 und AFMa273ye1	258	1236
35	im normalen Brustgewebe erhöht	Das humane "obese protein" (ob).		7q31.3	zwischen D7S686 und D7S530	237	749

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Ser. No.	Expression	Function
36	Elevated in normal breast tissue	The human Duffy-antigen (DARC gene).
37	Elevated in normal breast tissue	This protein has an approximately 50% amino acid identity with S3-12, a plasma membrane-associated protein, which is expressed during the fat cell differentiation.
38	Elevated in normal breast tissue	The human semaphorin E; it possibly mediates cellular resistance against cis-platinum (CDDP), a substance that is frequently used in chemotherapy.
39	Elevated in normal breast tissue	The human alpha-B-crystalline gene, originally cloned as a lens-specific gene, seems to be regulated by progesterone and estrogen in the endometrium. The expression correlates with the non-proliferative phase of the menstrual cycle.
40	Elevated in normal breast tissue	The human extracellular protein S1-5.
41	Elevated in normal breast tissue	The human lipoprotein-lipase.

I fd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
36	im normalen Brustgewebe erhöht	Das humane Duffy-Antigen (DARC-Gen).		1q22	zwischen D1S484 und D1S426	271	1251
37	im normalen Brustgewebe erhöht	Dieses Protein hat eine ca. 50%ige Aminosäure-Identität zu S3-12, einem Plasma Membran-assoziiertem Protein, das während der Fettzellen-Differenzierung exprimiert wird.		unbekannt	unbekannt	199	3283
38	im normalen Brustgewebe erhöht	Das humane Semaphorin E; es vermittelt möglicherweise zelluläre Resistenz gegen cis-Platinum (CDDP), einer in der Chemotherapie häufig verwendeten Substanz.		7q11.23-q21.13	stSG30323; zwischen D7S660 und D7S524	240	2720
39	im normalen Brustgewebe erhöht	Das humane alpha-B-Crystallin-Gen, ursprüngl. als linsen-spezifisches Gen kloniert, scheint im Endometrium durch Progesteron und Östrogen reguliert zu werden. Die Expression korreliert mit der Nicht-proliferativen Phase des Menstruationszyklus.	"crystallin"-Domäne und "HSP20"-Domäne	11q23.1-q23.2	zwischen D11S1893 und D11S938	247	1036
40	im normalen Brustgewebe erhöht	Das humane extrazelluläres Protein S1-5.	"EGF_CA"-Domäne	2p11.1-12	zwischen D2S2371 und D2S388	265	2659
41	im normalen Brustgewebe erhöht	Die humane Lipoprotein-Lipase.	"Lipase"-Domäne	8p22-p23.1	zwischen D8S261 und D8S258	252	2939

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Ser. No.	Expression	Function
42	Elevated in normal breast tissue	The human sFRP ("secreted frizzled-related protein") plays a role in programmed cell death (apoptosis)
43	Elevated in normal breast tissue	Unknown
45	Elevated in normal breast tissue	This sequence is probably the human ortholog of a fat cell-specific gene of the mouse.
47	Elevated in normal breast tissue	The human placenta "copper monoamine oxidase."
48	Elevated in normal breast tissue	Unknown
48	Elevated in normal breast tissue	The human "ras-like protein."
50	Elevated in normal breast tissue	Unknown
51	Elevated in normal breast tissue	Unknown
53	Elevated in normal breast tissue	The YAP (Yes-associated protein); it binds to SH3-domains.

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
42	im normalen Brustgewebe erhöht	Das humane sFRP ("secreted frizzled-related protein") spielt eine Rolle beim programmierten Zelltod (Apoptosis).		8p11.21-p12	zwischen D8S1791 und D8S268	404	3670
43	im normalen Brustgewebe erhöht	unbekannt		10q23.32-q25.1	WI-14063	259	1025
45	im normalen Brustgewebe erhöht	Diese Sequenz ist wahrscheinlich das humane Ortholog eines Fettzellen-spezifischen Gens der Maus.		unbekannt	unbekannt	328	538
47	im normalen Brustgewebe erhöht	Die humane Plazenta "copper monamine oxidase".		17q12	SHGC-3147	256	360
48	im normalen Brustgewebe erhöht	unbekannt	"HSP20"-Domäne	1p36.13-p36.23	zwischen D1S434 und D1S507	157	2192
49	im normalen Brustgewebe erhöht	Das humane "ras-like protein".	"ras"-Domäne	2p16.3-p21	zwischen D2S391 und D2S123	305	2952
50	im normalen Brustgewebe erhöht	unbekannt		7p12.1-p12.3	zwischen D7S506 und D7S659	188	615
51	im normalen Brustgewebe erhöht	unbekannt		11q12.1-q13.1	SHGC-35409; WI-7266 - D11S2006	290	1488
53	im normalen Brustgewebe erhöht	Das YAP (Yes-associated protein); es bindet an SH3-Domänen.		11q21.1-q22.3	D11S1339	289	2262

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Ser. No.	Expression	Function
54	Elevated in normal breast tissue	The human B4-2 protein.
56	Elevated in normal breast tissue	The human "long-chain acyl-CoA synthetase."
57	Elevated in normal breast tissue	The "prepro-melanine-concentrating hormone."
58	Elevated in normal breast tissue	Unknown
59	Elevated in normal breast tissue	A possible new member of the human tob-gene family.
60	Elevated in normal breast tissue	Unknown
61	Elevated in normal breast tissue	The human ortholog to the kryn gene of the mouse.
62	Elevated in normal breast tissue	Unknown

[Key:]

Domäne = domain

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
54	im normalen Brustgewebe erhöht	Das humane B4-2 Protein.		6q16.2	SHGC-31472	306	1301
56	im normalen Brustgewebe erhöht	Die humane "Lange Ketten Acyl-CoA Synthetase".		4q33-q35.2	zwischen D4S408 und D4S426	269	1265
57	im normalen Brustgewebe erhöht	Das "Prepro-Melanin-konzentrierende Hormon (prepro-melanin-concentrating hormone)".		12q22	AFM263ZD1; zwischen SHGC-15767 und SHGC-9350	247	274
58	im normalen Brustgewebe erhöht	unbekannt		2q22.3-2q23.2	SHGC-36777	270	2073
59	im normalen Brustgewebe erhöht	Ein mögliches neues Mitglied der humanen tob-Genfamilie.		21q11.1-q21.1	SHGC-11705; zwischen D21S1886 und D21S1256	205	850
60	im normalen Brustgewebe erhöht	unbekannt		1q22	SHGC-36663; zwischen SGC32839 und D1S1576	229	2091
61	im normalen Brustgewebe erhöht	Das humane Ortholog zum Kryn-Gen der Maus.	"SH3"-Domäne	4q31.3	SHGC-31182	225	2952
62	im normalen Brustgewebe erhöht	unbekannt		11p15.3	AFM166zel; zwischen SHGC-5993 und SHGC-13819	223	2313

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Ser. No.	Expression	Function
63	Elevated in normal breast tissue	Unknown
64	Elevated in normal breast tissue	The human ortholog to UMP-CMP kinase of the pig.
65	Elevated in normal breast tissue	Unknown
66	Elevated in normal breast tissue	The human cAMP phosphodiesterase.
67	Elevated in normal breast tissue	The human antigen CD 36.
68	Elevated in normal breast tissue	Presumably a human ortholog of the yeast <i>S. pombe</i> sad1 + gene.
69	Elevated in normal breast tissue	Unknown
71	Elevated in normal breast tissue	A new human protein, which contains an SH3-domain. These proteins are mediators of the intercellular cell communication.

[Key:]

Domäne = domain

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
63	im normalen Brustgewebe erhöht	unbekannt		2q24.1-q24.3	SHGC-1305; zwischen CHLC.GATA22H09 und WI-7620	192	1650
64	im normalen Brustgewebe erhöht	Das humane Ortholog zur UMP-CMP Kinase des Schweins.	"Adenylate-kinase"	1p32.3-p36.12	SHGC-36697; zwischen D1S2843 und D1S417	223	2851
65	im normalen Brustgewebe erhöht	unbekannt		4p15.1	WI-15951; zwischen D4S1043 und SHGC-16179	221	1071
66	im normalen Brustgewebe erhöht	Die humane cAMP Phosphodiesterase.	"PDEase"	8q13.1	CHLC.GATA86D08; zwischen SHGC-9281 und AFMa084wc5	199	2375
67	im normalen Brustgewebe erhöht	Das humane Antigen CD 36.	"CD36"-Domäne	7q11.23	sWSS1455	221	1823
68	im normalen Brustgewebe erhöht	Vermutlich ein humanes Ortholog des Hefe <i>S. pombe</i> sad1+ Gens.		7p22.3	SHGC-34866; zwischen SHGC-10715 und SHGC-32510	248	2403
69	im normalen Brustgewebe erhöht	unbekannt		5p15.33	zwischen D5S477 und D5S426	230	1246
71	im normalen Brustgewebe erhöht	Ein neues humanes Protein, das eine SH3-Domäne enthält. Diese Proteine sind Mediatoren der interzellulären Zellkommunikation.		8p21.3	SHGC-30970	263	1950

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Ser. No.	Expression	Function
72	Elevated in normal breast tissue	A new human gene, which possibly represents a transcription factor; a certain sequence identity with the DNA-binding protein CROC-1A exists on the nucleic acid plane.
74	Elevated in normal breast tissue	Presumably the human ortholog of the mouse Sox-18. The Sox proteins represent an important group of transcription factors that control development processes. Sox-genes have a so-called HMG-box ("high mobility group"). Mouse-Sox 18 is related to Sry ("testis-determining factor") of the human.
76	Elevated in normal breast tissue	Unknown

[Key:]

unbekannt = unknown

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
72	im normalen Brustgewebe erhöht	Ein neues humanes Gen, das möglicherweise einen Transkriptionsfaktor darstellt; auf Nukleinsäure-Ebene besteht eine gewisse Sequenzidentität zu dem DNA-bindenden Protein CROC-1A.		7q21.11-q22.1	R06442; zwischen D7S524 und D7S657	240	814
74	im normalen Brustgewebe erhöht	Vermutlich das humane Ortholog des Maus Sox-18. Die Sox-Proteine stellen eine wichtige Gruppe von Transkriptionsfaktoren dar, die Entwicklungsprozesse steuern. Sox-Gene weisen eine sog. HMG-Box ("high mobility group") auf. Maus-Sox 18 ist verwandt mit Sry ("testis-determining factor") des Menschen.		unbekannt	unbekannt	264	747
76	im normalen Brustgewebe erhöht	unbekannt		17p13.3-q25.3	AFM163yg1	296	2419

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Ser. No.	Expression	Module
161	Elevated in normal breast tissue	Lengthening to Seq. ID No. 1
162	Elevated in normal breast tissue	Lengthening to Seq. ID No. 4
163	Elevated in normal breast tissue	Lengthening to Seq. ID No. 10
164	Elevated in normal breast tissue	Lengthening to Seq. ID No. 11
165	Elevated in normal breast tissue	Lengthening to Seq. ID No. 12

[Key:]

Domäne = domain

unbekannt = unknown

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
161	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.1	"RGS"-Domäne; "ATP-synt_B"-Domäne; "TPR_Region TPR repeat"; "NLS_BP Bipartite nuclear localization signal"	unbekannt	unbekannt	205	3096
162	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.4	"CNH"-Domäne; "NLS_BP Bipartite nuclear localization signal"	Xq24	SHGC-14021 alias DXS9764	256	1987
163	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.10		3p24.3-p25.1	zwischen D3S1597 und D3S1263	310	1107
164	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.11	"TK"-Domäne	17q22-q23.2	SHGC-32689; zwischen D17S787 und D17S792	239	1062
165	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.12	"Polyoma_coat2"-Domäne	2q34	SHGC-3316; zwischen D2S315 und D2S2237	241	2770

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Domäne = domain
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Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
166	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.15	LIM; Ran_BP1; NLS_BP Bipartite nuclear localization signal	4p14	SHGC4-435; zwischen SHGC4-259 und SHGC-33782	228	4242
167	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.19	"UPF0024"-Domäne	1p22.1-p22.2	SHGC-34523	287	2640
168	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.22		10p15.1-p15.3	SHGC-16603; zwischen SHGC-16603 und SHGC-33903	288	1558
169	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.23		11q14.2-q14.3	zwischen D11S1354 und D11S931	204	1388
170	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.24	"ribonuclease_T2"-Domäne	10p15.1-p15.3	zwischen D10S591 und D10S189	291	2416
171	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr 25	"TK"-Domäne	2q35	AFM249wg9; zwischen CHLC.GATA29E02 und WI-7744	286	2720
172	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.38	"ig"-Domäne	7q11.23-q21.13	stSG30323; zwischen D7S660 und D7S524	240	2987
173	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.50		7p12.1-p12.3	zwischen D7S506 und D7S659	188	892

Ser. No.	Expression	Function
174	Elevated in normal breast tissue	Lengthening to Seq. ID No. 51
175	Elevated in normal breast tissue	Lengthening to Seq. ID No. 60
176	Elevated in normal breast tissue	Lengthening to Seq. ID No. 61
177	Elevated in normal breast tissue	Lengthening to Seq. ID No. 72
178	Elevated in normal breast tissue	Unknown

[Key:]

Domäne = domain

zwischen...und = between...and

Lfd. Nr.	Expression	Funktion	Module	Chromosomale Lokalisation	nächste Marker	Länge EST (bp)	Länge der angemeldeten Sequenz (bp)
174	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.51	"NLS_BP Bipartite nuclear localization signal"	11q12.1-q13.1	SHGC-35409; zwischen WI-7266 und D11S2006	290	1679
175	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.60	"NLS_BP Bipartite nuclear localization signal"	1q22	SHGC-36663; zwischen SGC32839 und D1S1576	229	2411
176	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.61	"SH3"-Domäne; "IL-6"-Domäne; "toxin_2"-Domäne	4q31.3	SHGC-31182	225	3450
177	im normalen Brustgewebe erhöht	Verlängerung zu Seq. ID Nr.72		7q21.11-q22.1	R06442; zwischen D7S524 und D7S657	240	874
178	im normalen Brustgewebe erhöht	unbekannt	"PH"-Domäne	9q34.11-q34.12	stSG3880; zwischen D9S1821 und D9S159	242	3265

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TABLE II

DNA Sequences
Seq. ID. No.

Peptide Sequences
Seq. ID. No.

1	77
2	78
	79
	80
	81
3	82
4	83
5	84
10	85
11	87
12	88
13	89
14	90
15	91
18	92
19	93
21	95
22	96
23	97
24	98
	99
25	100
	101
	102
	103
28	104

000260" 69594950

DNA Sequences
Seq. ID. No.

Peptide Sequences
Seq. ID. No.

30	105
	106
	107
31	108
34	112
37	113
42	114
43	115
	116
	117
45	119
48	122
50	124
	125
51	126
53	128
54	129
57	131
58	132
	133
59	135
60	137
61	138
62	139
	140
	141
63	142
	143
	144
	145
64	146
65	147
68	148
69	149
	150
71	151
72	152
	153
	154
	155
	156
74	157
76	158
	159
	160

000260" 69594960

DNA Sequences
Seq. ID. No.**Peptide Sequences**
Seq. ID. No.

161

162

163

164

165

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167

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The inventive nucleic acid sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178 of the determined candidate genes and the determined amino acid sequences Seq. ID No. 77 to Seq. ID No. 160 and Seq. ID No. 179 to Seq. ID No. 209 are described in the following sequence protocol.

Sequence Protocol

(1) GENERAL INFORMATION:

(i) APPLICANT

- (A) NAME: metaGen - Gesellschaft für Genomforschung mbH
- (B) STREET: Ihnestrasse 63
- (C) CITY: Berlin
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): D-14195
- (G) TELEPHONE: (030)-8413 1672
- (H) FAX: (030)-8413 1671

(ii) TITLE OF INVENTION: Human Nucleic Acid Sequences from Breast Tissue

(iii) Number of sequences: 183

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: Patentin release #1.0, version #1.25 (EPO)

000260" 69594960

(2) INFORMATION ON SEQ ID NO. 1:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2031 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69994960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATTGCATCAG	CCCGCCTGGA	AGAAGTCACT	GGGAAGCTAC	AAGTAGCTCG	GAACCTTATC	60
ATGAGGGGGA	CGGAGATGTG	CCCCAAGAGT	GAAGATGTCT	GGCTGGAAGC	AGCCAGGTTG	120
CAGCCTGGGG	ACACAGCCAA	GGCCGTGGTA	GCCCAAGCTG	TCCGTCATCT	CCCACAGTCT	180
GTCAGGATTT	ACATCAGAGC	CGCAGAGCTG	GAAACGGACA	TTCGTGCAAA	GAAGCGGGTT	240
CTTCGGAAAAG	CCCTCGAGCA	TGTTCCAAAC	TCGGTTCGCT	TGTGGAAAAGC	AGCCGTTGAG	300
CTGGAAGAAC	CTGAAGATGC	TAGAATCATG	CTGAGCCGAG	CTGTGGAGTG	CTGCCCCACC	360
AGCGTGGAGC	TCTGGCTTGC	TCTGGCAAGG	CTGGAGACCT	ATGAAAATGC	CCGCAAGGTC	420
TTGAACAAGG	CGCGGGAGAA	CATTCTTACA	GACCGACATA	TCTGGATCAC	GGCTGCTAAG	480
CTGGAGGAAG	CCAATGGGAA	CACGCAGATG	GTGGAGAAGA	TCATCGACCG	AGCCATCACC	540
TCGCTGCGGG	CCAACGGTGT	GGAGATCAAC	CGTGAGCAGT	GGATCCAGGA	TGCCGAGGAA	600
TGTGACAGGG	CTGGGAGTGT	GGCCACCTGC	CAGGCCGTCA	TGCGTGCCGT	GATTGGGATT	660
GGGATTGAGG	AGGAAGATCG	GAAGCATACC	TGGATGGAGG	ATGCTGACAG	TTGTGTAGCC	720
CACAATGCCC	TGGAGTGTGC	ACGAGCCATC	TACGCCTACG	CCCTGCAGGT	GTTCCCCAGC	780
AAGAAGAGTG	TGTGGCTGCG	CGCCGCGTAC	TTGAGAAAGA	ACCATGGCAC	TCGGGAGTCC	840
CTGGAAGCAC	TCCTGCAGAG	GGCTGTGGCC	CACTGCCCCA	AAGCAGAGGT	GCTGTGGCTC	900
ATGGGCGCCA	AGTCCAAGTG	GCTGGCAGGG	GATGTGCCTG	CAGCAAGGAG	CATCCTGGCC	960
CTGGCCTTCC	AGGCCAACCC	CAACAGTGAG	GAGATCTGGC	TGGCAGCCGT	GAAGCTGGAG	1020
TCCGAGAATG	ATGAGTACGA	GCGGGCCCCG	AGGCTGCTGG	CCAAGGCGCG	GACAGTGCCC	1080
CCACCGCCCC	GGTGTTCATG	AAGTCTGTGA	AGCTGGAGTG	GGTGCAAGAC	AACATCAGGG	1140
CAGCCCAAGA	TCTGTGCGAG	GAGGCCCTGC	GGCACTATGA	GGACTTCCCC	AAGCTGTGGA	1200
TGATGAAGGG	GCAGATCGAG	GAGCAGAAGG	AGATGATGGA	GAAGGCGCGG	GAAGCCTATA	1260
ACCAGGGGTT	GAAGAAGTGT	CCCCACTCCA	CACCCCTGTG	GCTTTTGCTC	TCTCGGCTGG	1320
AGGAGAAGAT	TGGGCAGCTT	ACTCGAGCAC	GGGCCATTTT	GGAAAAGTCT	CGTCTGAAGA	1380
ACCCAAAGAA	CCCTGGGCTG	TGGTTGGAGT	CCGTGCGGCT	GGAGTACCGT	GCGGGGCTGA	1440
AGAACATCGC	AAATACACTC	ATGGCCAAGG	CGCTGCAGGA	GTGCCCCAAC	TCCGGTATCC	1500
TGTGGTCTGA	GGCCATCTTC	CTCGAGGCAA	GGCCCCAGAG	GAGGACCAAG	AGCGTGGATG	1560
CCCTGAAGAA	GTGTGAGCAT	GACCCCCATG	TGCTCCTGGC	CGTGGCCAAG	CTGTTTTGGA	1620
GTCAGCGGAA	GATCACCAAG	GCCAGGGAGT	GGTCCACCG	CACTGTGAAG	ATTGACTCGG	1680
ACCTGGGGGA	TGCCTGGGCC	TTCTTCTACA	AGTTTGAGCT	GCAGCATGGC	ACTGAGGAGC	1740
AGCAGGAGGA	GGTGAGGAAG	CGCTGTGAGA	GTGCAGAGCC	TCGGCATGGG	GAGCTGTGGT	1800
GCGCCGTGTC	CAAGGACATC	GCCAACTGGC	AGAAGAAGAT	CGGGGACATC	CTTAGGCTGG	1860
TGGCCGGCCG	CATCAAGAAC	ACCTTCTGAT	TGAGCGGTTG	CCATGGCCGG	TCTCCGTGGG	1920
GCAGGGTTGG	GCCGCATGTG	GAAGGGCTCT	GAGCTGTGTC	CTCCTTCATT	AAAAGTTTTT	1980
ATGTCTCGTG	TCAGAAAAAA	AAAGAAAAAG	AAAAAGGGGG	CGCCCGGGGG	C	2031

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(2) INFORMATION ON SEQ ID NO. 2:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1081 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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AAGACCCCGT CTCTACAAAG CAAAACGAAA AACAACAAAT GGAGTTGTGC TATGTTGTAT 60
TGCTTTGCAC AAAATTAGGA ACAGGTGTTT GACAATTGAA TTTGTTTTCT GTGAATTCTA 120
ACCTCTAAAG GCATGCTTAG AGGTCAAGGA CCTTCCTGTG TAGTTGGTGC AAAAGCAATC 180
TCCACAGGAC AGCACTGCTT CCATGCTTCA TACATCAGGA AATGAGGCCA GAACTTGAGT 240
ATTTACTAAC ACGTTTTTCA AAAGATGTCA GTGTTATACC TAAAGCTAAA AAAAAGCAAG 300
GGTTTGTGTCAT AGAGGGAACC TCTAAATAAT TTCAGGGGTA GGGGAGATGT TGTCAATAGG 360
AAATGGGATA AAATATCAAG AGACAATGAA AACACTGCCT TGACATGAGG ACCAGCAAGT 420
TTATTCTTTT CATTTTCAGT GATGTTGGGA ATGGACTGGG TTTTAAAGG GAGCTTGAAG 480
AGGGAATGTT TGACAGTCAC AGAAGGTTCC TGCAGCAGAT GCCTCTTTTA GCCATTTCTC 540
ATTTTTTTCC TCAAATTTTA CCTACTGAGG CTCAAGCCTT CACAGTGAGC TGATGGTCTC 600
TACAGGGGAG GGGAGTCTAG GGAATTTATT TGGTATTTGT AAGGCAAGAG GTGATTTCTC 660
TCTAATATAT CTGATTATT GCTCATTTAA AACTGTAAAG TCCAGTATAA TTTTCCCTGA 720
TATGAAAAAA TGTGCATTTT TTTCACCTAG CAACAAAGTA CCTTCTAATT TCCAATAGTC 780
CGTGAAAGTT GGGGCTGAAG TACCTAAGTG TGAATGTCTC TCCCGTTAAA CTGAGTGTAG 840
AAATCTGAAT TTTTAAAAGA GCTGTAAC TAAGTGAAGT CTTAGGAAGA AACTTTGCAA 900
ACATTTAATG AGGATACACT GTTCATTTT AAAATTCCTT CACACTGTAA TTTAATGTGT 960
TTTATATTCT TTTGTAGTAA AACAACATAA CTCAGATTTT TACAGGAGAC AGTGGTTTTA 1020
TTTGGATTGT CTTCTGTAAT AGGTTTCAAT AAAGCTGGAT GAACTTAAAA AAAAAAAAAA 1080
A

```

(2) INFORMATION ON SEQ ID NO. 3:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCCAAAGCGC AGGGTCAGCG ACACTTCTTC CGGCCCAACG CCGTGCATGG AGCCCATCCT 60
 GGGCCGCACG CATTACAGCC AGCTGCGCAA GAAGAGCTGA GTCGCCGCAC CAGCCGCCGC 120
 GCCCCGGGCC GCGGGGTTTC TCTAACAAAT AAACAGAACC CGCACTGCCC AGGCGAGCGT 180
 TGCCACTTTC AAAGTGGTCC CCTGGGGAGC TCAGCCTCAT CCTGATGATG CTGCCAAGGC 240
 GCACTTTTTA TTTTATTTT ATTTTATTT TTTTTTAGC ATCCTTTTGG GGCTTCACTC 300
 TCAGAGCCAG TTTTAAAGG ACACCAGAGC CGCAGCCTGC TCTGATTCTA TGGCTTGGTT 360
 GTTACTATAA GAGTAATTGC CTAAGTTGAT TTTTCATCTC TTTAACCAAA CTTGTGGCCA 420
 AAAGATATTT GACCGTTTCC AAAATTCAGA TTCTGCCTCT GCGGATAAAT ATTTGCCACG 480
 AATGAGTAAC TCCTGTCACC ACTCTGAAGG TCCAGACAGA AGGTTTTGAC ACATTCTTAG 540
 CACTGAATC CTCTGTGATC TAGGATGATC TGTTCCCCCT CTGATGAACA TCCTCTGATG 600
 ATCTAGGCTC CCAGCAGGCT ACTTTGAAGG GAACAATCAG ATGCAAAAGC TCTTGGGTGT 660
 TTATTTAAAA TACTAGTGCT ACTTTCTGAG TACCCGCCGC TTCACAGGCT GAGTCCAGGC 720
 CTGTGTGCTT TGTAGAGCCA GCTGCTTGCT CACAGCCACA TTTCCATTTG CATCATTACT 780
 GCCTTCACCT GCATAGTCAC TCTTTTGATG CTGGGGAACC AAAATGGTGA TGATATATAG 840
 ACTTTATGTA TAGCCACAGT TCATCCCCAA CCCTAGTCTT CGAAATGTGA ATATTTGATA 900
 AATCTAGAAA ATGCATTCAT ACAATTACAG AATTCAAATA TTGCAAAAGG ATGTGTGTCT 960
 TTCTCCCCGA GCTCCCCTGT TCCCCTTCAT TGAAAACCAC CACGGTGCCA TCTCTGTGT 1020
 ATGCAGGGCT ATGCACCTGC AGGCACGTGT GTATGCACTC CCCGCTTGTT TTTACACAAG 1080
 CTGTGGGGTG TTACGCATGC CTGCTTTTTT CACTTAATAA TACAGCTTGG AGAGATTTTT 1140
 GTATCACATT ATAAATCCCA CTCGCTCTTT TTGATGGCCA CATAATAACT ACTGCATAAT 1200
 ATGGATACGC CTTATTTGAT TTAAGTAGTT CCCTAATGAT GGACTTTTAA GTTGTTCCT 1260
 TTTTTTTTCT TTTTGTCTAC TGCAAACGAT GCTATAATAA ATGTCCTTAT CAAAAATG 1318

(2) INFORMATION ON SEQ ID NO. 4:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 731 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

09646569.092000

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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CTTGGGACAA GACTCTCACC AGCACATCAC ACACGTTCTC CTTGGAAGAG AGAAGCAGTA 60
CATCCCGGTT GAGAGGTCAC AAAGCATTAG TGGAAGAAAT GTGGTAAAGG GGGGAAGGTG 120
TTATGCGGCT GCTCCCTCCG TCCCAGAGGT GGCAGTGATT CCATAATGTG GAGACTAGTA 180
ACTAGATCCT AAGGCAAAGA GGTGTTTCTC CTTCTGGATG ATTCATCCCA AAGCCTTCCC 240
ACCCAGGTGT TCTCTGAAAG CTTAGCCTTA AGAGAACACG CAGAGAGTTT CCCTAGATAT 300
ACTCCTGCCT CCAGGTGCTG GGACACACCT TTGCAAAATG CTGTGGGAAG CAGGAGCTGG 360
GGAGCTGTGT TAAGTCAAAG TAGAAACCCT CCAGTGTGTTG GTGTTGTGTA GAGAATAGGA 420
CATAGGGTAA AGAGGCCAAG CTGCCTGTAG TTAGTAGAGA AGAATGGATG TGGTTCTTCT 480
TGTGTATTTA TTTGTATCAT AAACACTTGG AACAACAAAG ACCATAAGCA TCATTTAGCA 540
GTTGTAGCCA TTTCTAGTT AACTCATGTA AACAAGTAAG AGTAACATAA CAGTATTACC 600
CTTTCAGTGT TCTCACAGGA CATGTACCTA ATTATGGTAC TTATTTATGT AGTCACTGTA 660
TTTCTGGATT TTAAATTAA TAAAAAAGTT AATTTTGAAA AATCAAAAAA AAAAGAAAGG 720
AAGTAAAAGG A 731

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(2) INFORMATION ON SEQ ID NO. 5:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2719 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGAGACCAGG	CCCACAGAGA	ACAGGGCAAG	GAGCAGGCCA	TGTTTGATAA	GAAGGTGCAG	60
CTCCAGAGAA	TGGTAGACCA	AAGGTCGGTG	ATTTTCAGATG	AAAAGAAAGT	TGCCCTCCTC	120
TATCTAGACA	ATGAGGAGGA	GGAGAATGAT	GGGCATTGGT	TTTAATAAGC	AGAAACATTT	180
TGTTTTAATG	GCAGCCTGTT	GGCGACGTGC	CAACATCCAA	AGGCCTTAAC	TTATTTTAAG	240
AGGCCGAGGG	AGTCTATGAA	AATCTCCCCT	TTTTTACTTT	TTTAAAGAGT	ACTCCCGGCA	300
TGGTCAATTT	CCTTTATAGT	TAATCCGTAA	AGGTTTCCAG	TTAATTCATG	CCTTAAAAGG	360
CACTGCAATT	TTATTTTTGA	GTTGGGACTT	TTACAAAACA	CTTTTTTCCC	TGGAGTCTTC	420
TCTCCACTTC	TGGAGATGAA	TTTCTATGTT	TTGCACCTGG	TCACAGACAT	GGCTTGCATC	480
TGTTTGAAAC	TACAATTAAT	TATAGATGTC	AAAACATTAA	CCAGATTAAA	GTAATATATT	540
TAAGAGTAAA	TTTTGCTTGC	ATGTGCTAAT	ATGAAATAAC	AGACTAACAT	TTTAGGGGAA	600
AAATAAATAC	AATTTAGACT	CTAAAAAGTC	TTTTCAAAAA	GAAATGGGAA	ATAGGCAGAC	660
TGTTTATGTT	AAAAAAATTC	TTGCTAAATG	ATTTCATCTT	TAGGAAAAAA	TTACTTGCCA	720
TATAGAGCTA	AATTCATCTT	AAGACTTGAA	TGAATTGCTT	TCTATGTACA	GAACCTTAAA	780
CAATATAGTA	TTTATGGCGA	GGACAGCTGT	AGTCTGTTGT	GATATTTTAC	ATTCTATTTG	840
CACAGGTTCC	CTGGCACTGG	TAGGGTAGAT	GATTATTGGG	AATCGCTTAC	AGTACCATTT	900
CATTTTTTGG	CACTAGGTCA	TTAAGTAGCA	CACAGTCTGA	ATGCCCTTTT	CTGGAGTGGC	960
CAGTTCCTAT	CAGACTGTGC	AGACTTGCGC	TTCTCTGCAC	CTTATCCCTT	AGCACCCAAA	1020
CATTTAATTT	CACTGGTGCG	AGGTAGACCT	TGAAGACAAT	GAAGAGAATG	CCGATACTCA	1080
GACTGCAGCT	GGACCGGCAA	GCTGGCTGTG	TACAGGAAAA	TTGGAAGCAC	ACAGTGGACT	1140
GTGCCTCTTA	AAGATGCCTT	TCCCAACCCCT	CCATTTCATGG	GATGCAGGTC	TTTCTGAGCT	1200
CAAGGGTGAA	AGATGAATAC	AATAACAACC	ATGAACCCAC	CTCACGGAAG	CTTTTTTTGC	1260
ACTTTGAACA	GAAGTCATTG	CAGTTGGGGT	GTTTTGTCCA	GGGAAACAGT	TTATTAAATA	1320
GAAGGATGTT	TTGGGGAAGG	AACTGGATAT	CTCTCCTGCA	GCCCAGCACC	GAGATACCCA	1380
GGACGGGCCCT	GGGGGGCGAG	AAAGGCCCCC	ATGCTCATGG	GCCGCGGAGT	GTGGACCTGT	1440
AGATAGGCAC	CACCGAGTTT	AAGATACTGG	GATGAGCATG	CTTCATTGGA	TTCAATTTAT	1500
TTTACACGTC	AGTATTGTTT	TAAAGTTTCT	GTCTGTAAAG	TGTAGCATCA	TATATAAAAA	1560
GAGTTTCGCT	AGCAGCGCAT	TTTTTTTAGT	TCAGGCTAGC	TTCTTTCACA	TAATGCTGTC	1620
TCAGCTGTAT	TTCCAGTAAC	ACAGCATCAT	CGCACTGACT	GTGGCGCACT	GGGGAATAAC	1680
AGTCTGAGCT	AGCACCAACC	TCAGCCAGGC	TACAACGACA	GCACTGGAGG	GTCTTCCCTC	1740
TCAGATTAC	CTGGAGGCC	TCAGACCCCC	AGGGTGCACG	TCTCCCCAGG	TCCTGGGAGT	1800
GGCTACCGCA	GTAGTTTCTG	GAGAGCACGT	TTTCTTCATT	GATAAGTGGA	GGAGAAATGC	1860
AGCACAGCTT	TCAAGATACT	ATTTTAAAAA	CACCATGAAT	CAGATAGGGA	AAGAAAGTTG	1920
ATTGGAATGG	CAAGTTTAAA	CCTTTGTTGT	CCATCTGCCA	AATGAACTAG	TGATTGTCAG	1980
ACTGGTATGG	AGGTGACTGC	TTTGTAAGGT	TTTGTCGTTT	CTAATACAGA	CAGAGATGTG	2040
CTGATTTTGT	TTTAGCTGTA	ACAGGTAATG	GTTTTTGGAT	AGATGATTGA	CTGGTGAGAA	2100
TTTGGTCAAG	GTGACAGCCT	CCTGTCTGAT	GACAGGACAG	ACTGGTGGTG	AGGAGTCTAA	2160
GTGGGCTCAG	TTTGATGTCA	GTGTCTGGGC	TCATGACTTG	TAAATGGAAG	CTGATGTGAA	2220
CAGGTAATTA	ATATTATGAC	CCACTTCTAT	TTACTTTGGG	AAATATCTTG	GATCTTAATT	2280
ATCATCTGCA	AGTTTCAAGA	AGTATTCTGC	CAAAAGTATT	TACAAGTATG	GACTCATGAG	2340
CTATTGTTGG	TTGCTAAATG	TGAATCACGC	GGGAGTGAGT	GTGCCCTTCA	CACTGTGACA	2400
TTGTGACATT	GTGACAAGCT	CCATGTCCTT	TAAAATCAGT	CACTCTGCAC	ACAAGAGAAA	2460
TCAACTTCGT	GGTTGGATGG	GGCCGGAACA	CAACCAGTCT	TTTTGTATTT	ATTGTTACTG	2520
AGACAAAACA	GTAATCACTG	AGTGTTTTTT	AGTTTCCTAC	TGGTGGTTTT	GATATTGTTT	2580
GTTTAAGATG	TATATTTAGA	ATGACATCAT	CTAAGAAGCT	GATTTTGCTA	AACTCCTGTT	2640
CCCTACAATG	GGAAATGTCA	CAAGAATGTG	CAAAAATAAA	AATCTGAGGA	AAAAACCCAA	2700
AAAATTCCTA	AAGAGAATG					2719

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(2) INFORMATION ON SEQ ID NO. 10:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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gggccggggca gcccagctga aggcaataag ctgggctcac cgctgcagca gagttctgtg 60
ctagccgggc ataggggcga gagaaggccc agaggcgacg tcagagagaa gcaactgcgc 120
cccgggtgaag agaagctcgc ccatacccg ctgggagcca gctttcagtg aagatggcag 180
ggccagaact gttgcttgac tccaacatct gcctctgggt ggtcctaccc atcgttatca 240
ctcttcgtag acatgatccg ccactacgtg tccatcctgc tggagagcga caagaagctc 300
accaggaac aagtatctga caggggacga ggcacccaca gtccctctcc cataagcctg 360
ccaagaagat tgatgtggcc cgtgtaacgt ttgacctgta caagctgaac ccacaggact 420
tcattggctg cctgaacgtg aaggcgactt tttatgatac atactccctt tcctatgatc 480
tgcaactgctg tggggccaag cgcatacga aggaagcttt ccgctgggce ctcttcagca 540
tgcaggccac aggccacgta ctgcttgga cctcctgtta cctgcagcag ctcttcgatg 600
ctacggagga agggcagccc cccaagggca aggcctcatc ccttatcccg acctgtctga 660
agatactgca gtgaaagccc aagtccttgg aagctttccc cagtgaagga ctgactgggg 720
gcctcacgct taactggtag tgcccacaag cctggcagct gtagagccgc gaacctcccc 780
acacctccct caccgcgcag gaccctgagt gaggaggagg agctggaaac ctgggggtggg 840
ttggccaaag gagaacctca agctcctggc ctgatccagc tccttcctgc ccaaggcagc 900
ttagcccatc cagactgggtc ctgaagtctg tccctccatt ggcatgaagt ctgcccctca 960
gcagtccggc ctacacaggct gtactttcat ggtgctctct accttctggc ccccatccca 1020
gaacattcgt gagtgaattc gcaagcatat tagcatgtga tattaggag tttgcaataa 1080
attattgatg ctgatgtaaa aaaaaaa

```

1107

(2) INFORMATION ON SEQ ID NO. 11:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

09646569.092000

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

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gtgaatatgt gtgtatatgt gtgtgtatgt gtgtgtgggg tttggggtag aaggaggagga 60
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taagtgggct tttatgctaa aagcctctgg ggatatctgt tttgaaaata aagatagggtg 180
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tctgtgtttc cccctgccct ccagactgt gtggccagtt gaaagtgtct ggtttgtgtt 900
catctctccc tcatttcttg agcagggcct gagaccctgc cacatctcct atgctctgca 960
tccacgcctc ttttgacat taaagggttg ttgatgcaaa acaactttac aacgggggtg 1020
cttggggaag cctgggggtg gccggcttat ggggttgctg cg 1062

```

(2) INFORMATION ON SEQ ID NO. 12:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1471 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

09645569 "092000

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

attacaggca tgagccactg taccagcctt ttccttataa aattcaaaga gaaaatttct 60
acacctttat ccttcaaata aaacaagtgc tcagttctta ccgtgccctt gcaagggtcta 120
tatgtaaaag aaatctgaaa tttagctgta gaataaaact tgataaataa aaagaaaaaa 180
catacatttc tccagttggt ttgctctttg cttgttgaag taataaacgg ttttaaagag 240
aaaataacttg ctgtaaaccc ccagtgccctt caactctttt ggcagaatat ttttaaagaa 300
atccagcaag caaactttga ggtgctaata aaagtaaagg aagggtggtat ttctagtttt 360
ggcagaaatg aaaagtgtct cacaagagac atcactaccc acgtgggggtc tggctgcttt 420
ctaccaaaga catttagaga agaagtgaat tgagtcaggg tgatggtgaa cactacatat 480
tttatagatg gtttaagtga gaattaatta tgtttatcat ggatggctac taataccaag 540
ctcatgattg ttgcagcctc aacgtcttag gcagtaaac ttgtctgcag cactaaaggg 600
ggagaaaccc ttatatattg caaactgtcc attcggtaaa tttattgtaa cctaatacca 660
aaaactgccg tttttcatat tatttcccca cctcctactt tttttttttt tttttgctac 720
ttgtaaaata accccttcta gaaaataagc attaactgga atgtttcaaa caattttgct 780

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tcattttact atcagccact agtgaactct tacagagatg tacatttaag ataaaattag 840
cttgtgctaa gtgtttttaa aacattgttt actgttaaag ggaattgca cattatat 900
aactgggatt gctccctccc tcagttcttt aaaaaacaag agtcaaggct cacaccaact 960
tgtaggctgt gggagctttg ccattaggtg atacaatgta gaagtatact tttttaaagc 1020
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attatgcaca gtcagtgaa gatgaagtta caatttttct cgcagctttg ttgctattat 1140
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cttatatata tatatatata gatagataga tagatagata gatatatgag agagatatat 1260
tcagtactac tgaggatggt tttctgagga tgtttttgtt ctgctggatt aagttatttt 1320
ccaagttact cttgccagtt atgtcagtaa actattgtaa tggcttagca cactagtcgt 1380
acagtcagtg taaatgtttt tcattttacat gttttcatta tatcagctta tcaaatcctt 1440
aataaaaaaa attcatagat ttcattttaa c

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1471

(2) INFORMATION ON SEQ ID NO. 13:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2738 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

000260"6954960

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

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gctccgtgcc agcatgctac cctgggaggc acatccaggc ttgggaaacg ggggtgtcct 60
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ccccccccac ttgggtgttt ttgtttgttt tagcaattca gagctcaaga taaagacctt 180
aaagataact ttgtgtgtct ctccttttct aggtatttgc ataggaatca gaggagttaa 240
tcttgtctct tctcacaggt ttgaatcttc agacaaactt ctgggaggac tccgtccatg 300
cctcgagcga gatgttccct gtcaatcagt aggc aaattg gctacccatt ctcccagaa 360
atctcaccag tgtgctcact gtgagaagac gttcaaccgg aaagaccacc tga aaaacca 420
cctccagacc caccagccca acaaaatggc ctttgggtgt gaggagtgtg ggaagaagta 480
caacaccatg ctgggtcata agaggcacct ggccctccat gcggccagca gtggggacct 540
cacctgtggg gtctgtgccc tggagctagg gaggaccgag gtgctactgg accacctcaa 600
agcccatgcg gaagagaagc cccctagcgg aaccaaggaa aagaagcacc agtgcgacca 660
ctgtgaaaga tgcttctaca cccggaaggga tgtgcgacgc cacctgggtg tccacacagg 720
atgcaaggac ttctgtgccc agttctgtgc ccagagattt gggcgcaagg atcacctcac 780
ccggcatacc aagaagaccc actcacagga gctgatgaaa gagagcttgc agaccggaga 840
ccttctgagc accttcaca ccattctgcc ttcattccaa ctgaaggctg ctgccttgcc 900
tcctttccct ttaggagctt ctgcccagaa cgggcttgca agtagcttgc cagctgaggt 960

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ttattcagtg atgactggct tgagatgata agagaattct cgaactgcat gtattgtgcc1740
aatctgtcct gagtgttcat gctttgtacc aaatttaatg aacgcgtgtt ctgtaatcaal800
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acatacatat tttcttgttg agcaatagag ttctccattt tacagaagca ttttaaatgt2160
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aacaagaatt ttctttgtct tgtctagctt aaactactac tcaagctgct taagttctta2460
agtattgttt gtaatcacca ataaataagt gcattttgaa ttcacagctc attattagct2520
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ttaatgagtt ttaaagatgt aaaacctaac cttttttaa gctccattgt cttatgtttt2640
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2738

09646569.092000

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

- (A) ORGANISM: HUMAN
(C) ORGAN:

- (A) LIBRARY: cDNA library

cgccgcggcc	cctcctccca	gagcggcagc	cttttccgc	gcgtgtgcc	ttcgccgtc	60
gggcccgcg	ggggaaaaca	tggcgtctgc	cctggagcag	ttcgtgaaca	gtgtccgaca	120
gctctcagct	caagggcaaa	tgacacagct	ttgtgaactg	atcaacaaga	gtgggggaact	180
ccttgcgaa	aacttatccc	atctggacac	tgtgtctcggg	gctctggatg	tacaagaaca	240
ctccttgggc	gtccttgc	ttttgtttgt	gaagttttct	atgcccagtg	ttcctgactt	300
cgaaacgcta	ttctcacagg	ttcagctctt	catcagcact	tgtaatgggg	agcacattcg	360
atatgcaaca	gacacttttg	ctgggctttg	ccatcagcta	acaaatgcac	ttgtggaaaag	420
aaaacagtga	caacataaga	tccaatgtgc	tgccatcttt	gagaacttat	ctgaaagaga	480
tgtcatttct	gacagccctt	gcgaggaatt	ggcatcctta	agcaagccat	agacaagatg	540
cgatgaata	caaacacagct	gacctcaata	catgctgac	cttgcagct	ttgtttgcta	600
gcaaaatgct	ttaagcctgc	ccttccatat	cttgacgtgg	atatgatgga	tatctgtaaa	660
gagaatggag	cctatgatgc	aaaacacttt	ttatgttact	attattatgg	agggatgatc	720
tatactgggc	tgaagaactt	tgaagagct	ctctactttt	atgaacaggc	tataactact	780
cctgccatgg	cggtcagtc	tatcatgttg	gaatcatata	aaaagtatat	tttagtgtct	840
ttgatattac	ttggcaaaagt	acaacagcta	ccaaaatata	catctcaa	tgtgggtaga	900
ttcattaagc	ctcttagcaa	tgcataccac	gagttagcac	aagtgtattc	aaccaacaac	960
ccctcagaac	tccgaaacct	ggtgaataag	cacagtga	ccttcactcg	cgataacaac	1020
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aagacctttt	taactctatc	attacaagat	atggcaagtc	gtgtgcagtt	gtctggacct	1140
caggaggcag	agaaatacgt	tctgcacatg	atagaagatg	gtgagatttt	tgcaagtatt	1200
aaccagaagg	acggtatggt	cagtttccat	gataaccctg	aaaaatataa	taaccagacc	1260
atgcttcata	acattgatca	ggagatgctg	aagtgcattg	agctggatga	gcggctgaaa	1320
gccatggacc	aggagatcac	agtgaaccct	cagtttgtac	aaaagagtat	gggctcaca	1380
gaagatgatt	caggaaacaa	accatccagt	tattcttgaa	actaacatcc	atcctgagct	1440
aaacaagaga	aactaccatc	ttggccagtg	acaagtgttc	ggaggggcagc	agagaggacc	1500
aagccttgtg	cacctggaga	ctaagaaatt	aagttttgtt	ttgacatctt	cagtcctgtg	1560
tgtcttcaga	aaaccattttt	ctcgtcaaa	aaaggaaaca	gatttgcaa	ctttaaagtc	1620
tgctcgtggat	ttatttatcc	tcagattatt	gttactgc	taaatctacc	tttttgtttt	1680
aagttgcttg	aacattaaaa	aaaaaaaaaa				1710

(2) INFORMATION ON SEQ ID NO. 15:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3159 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

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cgctggataa aagcattaac catcagatcg agtctcccag tgaaaggcgg aagtctataa 60
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tcgagaccct caatctctat tttcacatcc agtgtttcag gtgtggaatt tgtaaaggcc 180
agcttgagga tgcagtgagt gggacggatg ttaggattcg aaatgggtctc ctgaactgta 240
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aagcttcggg atcactcacc atttctttac tgagagtgtc ccctggcaac tgcttaacaa 360
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cttctttggg aattagctaa atgatgcaat aaacctgttt tgttttagaa tgtctaggaa 660
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caagctctat ctctgagcta taatttgttt ttaatgcaaa gacactagtt tgataatata 840
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caagttctcc ttaagggcct gaagcacagg tgtccaaaga aaagcgtaa gtccatctta 1320
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ctagcgatta tttattacat gctagatggg ttctttgcat gtgggttcca tataggtgca 1860
gaaatttctc cagccactgg agggatttgc accatatattg tcatttggat gagctgttat 1920
tagattgaaa tctacacatc atttcattaa aaattgtgcc ttagaaaacg caaagctgtt 1980
gcacatggcg ataaattatg gatgcagtac attgaagaga gatgaagtca cttccaagtt 2040
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aaaaaaagag aaaaaattaa attcaaaaat tgttttgaaa atgtacagat caagtccaat 2160
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tgcatgatat tagcagagta ccactagtaa tgcacaaaca tgtacaatat ggtcattcat 2280
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ctcattgtac atgtattgaa gctagaatcg agtcaagaaa aataaagccc catttccaa 2460
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ggccagtgtt ctatatcggt tatactaact ttcatttata gtattttatt taaaatgcct 3060
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aatgtacatt tataaataaa atactcaaat caaaaaaaa 3159

```

09646569.092000

(2) INFORMATION ON SEQ ID NO. 16:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1680 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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accagcaatt gcagcactta caatcactaa ttcccttaag gttgaaactg taatgacata 420
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gaagaaatgc ctctatgtag gtgaagtgtt ctctctgcat gcaacagtaa aaattaatat 960
aatattttcc ccacaaaaga aacacttaac agaggcaagt gcaatttata aatttatatc 1020
taaaggggaa tcatgattat aagtccttca gcccttggac tctaaattga ggggattaaa 1080
aagaatttaa aataattttg aacgaattta ttttcccctc agtttttgag ggcattaaaa 1140
aggcattaaa tcaagacaaa tcatgtgctt gagaaaaata aaattaatga aaacacagca 1200
cttatgttgg tttagctgca gctccttgg aggtagaatt tatttattta aaattactgg 1260
ttgcatcaag aacctatagg gtgtacaaaa ggttctataa aatctgcatt atagagacaa 1320
agaggcaggc aaatccatgt cacaagggtt aagcttacag ttacaaaact gggaacgcc 1380
gggtgtagga tataaaaaacg cactcttgag aaaacaaatg taatcagggt gctgaaaact 1440
tgcatggtgc tttcagacat tagccttggt caacaaattt cttgtattga cagatccata 1500
gtgtgcatgg gcagacacat tttgcctcta tgtctcttaa aattttaatt aaaaatactc 1560
ttccagtaa tcctaatttg cacgaagata taatgtccac attacgtgcc ttgccttgaa 1620

atctaaaaaa caaaaaacaa aaaagaaaag gaacaaaaaa atacaacaaa gtgacatcac 1680

```


(2) INFORMATION ON SEQ ID NO. 18:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1722 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260 " 69594950

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

cattgtttgc caaaatccca ggcagcatgg acctcagctt tctctgggta cttctgcccc 60
 tagtcacccat ggcttggggc cagtattggc attatggata cccataccag cagtatcatg 120
 actacagcga tgatgggtgg gtgaatttga accggcaagg cttcagctac cagtgtcccc 180
 agggggcaggt gatagtggcc gtgaggagca tcttcagcaa gaaggaaggt tctgacagac 240
 aatggaacta cgcttgcatt cccacgccac agagcctcgg ggaacccacg gagtgtctgg 300
 gggaggagat caacagggct ggcattggaat ggtaccagac gtgctccaac aatgggctgg 360
 tggcaggatt ccagagccgc tacttcgagt cagtgtctga tcgggagtg cagttttact 420
 gttgtcgcta cagcaagagg tgcccatatt cctgtctggc aacaacagaa tatccaggtc 480
 actatggtga ggaaatggac atgatttctt acaattatga ttactatata cgaggagcaa 540
 caaccacttt ctctgcagtg gaaagggatc gccagtggaa gttcataatg tgccggatga 600
 ctgaatacga ctgtgaattt gcaaatgttt agatttgcca cataccaaat ctgggtgaaa 660
 ggaaaggggc cggggacagg aggggtgtcca catatgttaa catcagttgg atctcctata 720
 gaagtttctg ctgctctctt tcttctctcc tgagctggta actgcaatgc caacttctctg 780
 ggcttttctg actagtatca cacttctaataaaaatccaca attaaacat gtttctcact 840
 tttcacatgt ttcatagcaa ctgctttata tgactgatga tggcttctct gcacaccaca 900
 tatacagtcg gcattgctac agccgggctt ctggagcacc agctgcagcc tggctactgc 960
 tttttactgc agaatgaact gcaagttcag catagtggag gggagaggca gaactggagg 1020
 agaggtgcag tgaaggttct ctacagctaa gcctgtttga atgatacgta ggttccccac 1080
 caaaagcagg ctttctgccc tgagggacat cttccctact cctgtctcca catgagccat 1140
 gcatgcttag caatccaagt gcagagctct ttgctccagg agtgaggaga ctgggaggtg 1200
 aaatggggaa atggaagggt ttggaggcag agctgaaaac aggggttgaa ggatttctctg 1260
 aattagaaga caaacgttag catacccagt aaggaaaatg agtgcagggg ccaggggaaac 1320
 ccgtgaggat cactctcaaa tgagattaaa aacaaggaa cagagaatgg tcagagaatg 1380
 ggattcagat tgggaacttg tggggatgag agtgaccagg ttgaactggg aagtggaaaa 1440
 aggagtttga gtcactggca cctagaagcc tgccacagat tcctaggaag gctggcagac 1500
 accctggaac cctggggagc tactggcaaa ctctcctgga ttgggcctga tttttttggt 1560
 gggaaaggct gccctgggga tcaactttcc ttctgtgtgt ggctcaggag ttcttctgca 1620
 gagatggcgc tatcttttct cctcctgtga tgtcctgctc ccaaccattt gtactcttca 1680
 ttacaaaaga aataaaaaata ttaacgttca ctatgctgaa aa 1722

(2) INFORMATION ON SEQ ID NO. 19:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1612 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

096465569 092000

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

```

ggccatggaa attaaagttg aaaaagactt gaagactgga gaaagtacag ttctgtcttc 60
aattacctct gccatcagat gacttttaaag gtacaggaat aaaagtttat gatgatgggc 120
aaaagtcagt gtatgcagta agttctaata acagtgcagc atacaatggc accgatggcc 180
tggcaccagt tgaagtagag gaacttctaa gacaagcctc agagagaaac tctaaatccc 240
caacagagta tcatgagcct gtatatgcca atccctttta caggcctaca accccacaga 300
gagaaacggt gacccttgga ccaaactttc aagaaaggat aaagattaaa actaatggac 360
tgggtattgg tgtaaatgaa tccatacaca atatgggcaa tggcttttca gaggaaaggg 420
gaaacaactt caatcacatc agtcccattc cgccagtgcc tcatccccga tcagtgattc 480
aacaagcaga agagaagctt cacaccccg c aaaaaaggct aatgactcct tgggaagaat 540
cgaatgtcat gcaggacaaa gatgcacct ctccaaagcc aaggctgagc cccagagaga 600
caatatttgg gaaatctgaa caccagaatt cttcaccac ttgtcaggag gacgaggaag 660
atgtcagata taatatcggt cattccctgc ctccagacat aaatgataca gaaccgggtga 720
caatgatttt catgggggat cagcaggcag aagacagtga agaagataag aagtttctga 780
caggatatga tgggatcatc catgctgagc tggttgtgat tgatgatgag gaggaggagg 840
atgaaggaga agcagagaaa ccgtcctacc accccatagc tccccatagt cagggtgtacc 900
agccagccaa accaacacca ctctctagaa aaagatcaga agctagtctt catgaaaaca 960
caaatacata atccccccac aaaaattcca tatctctgaa agagcaagaa gaaagcttag1020
gcagccctgt ccaccattcc ccatttgatg ctgagacaac tggagatggg actgaggatc1080
catccttaac agctttaagg atgagaatgg caaagctggg aaaaaagggtg atctaagagt1140
tgtaccacct atataaacat ctttgaaga agaaactaag aagcatttgc aaatttctct1200
tctggatatt ttgtttattt tttctgaagt ccaaaaaatt atcattacag tgtaccatat1260
taagccatgt gaataagtag tagtcattat ttgtgaaaaa ttccccaaaaa gctgggggaaal320
acaaatgtgt aacttttcca gttacttgac acgattcagt ggggggaaaac cagcattttt1380
tattctattg ataccaaagc atttctaata agagcttggt aaatttaaga ataaagttat1440
ttaaaatata aagagtatag tatattaact ggcattgtaa ttttgatgat acaaagattg1500

aaagatcata ggaaagcatt gcccttcac acagaagtat tcaactctga caaataaatal560
tgtcatcctg aattaaataa gccttaataa aagtacatcc tctgctaaa aa 1612

```

(2) INFORMATION ON SEQ ID NO. 21:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1304 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

000260" 69594960

(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```

agaagttccc aggcatacgg cttacctgg ctacactggc aggcaacttc cgaatgcctg 60
tggtgaggga gtacctgatg tctggaggta tctgccctgt cagccgggac accatagact 120
atttgctttc aaagaatggg agtggcaatg ctatcatcat cgtggtcggg ggtgcggtg 180
agtctctgag ctccatgcct ggcaagaatg cagtcaccct gcggaaccgc aagggctttg 240
tgaaactggc cctgcgtcat ggagctgacc tggttcccat ctactccttt ggagagaatg 300
aagtgtacaa gcagggtgatc ttcgaggagg gctcctgggg ccgatgggtc cagaagaagt 360
tccagaaata cattggtttc gccccatgca tcttccatgg tcgaggcctc ttctcctccg 420
acacctgggg gctggtgccc tactccaagc ccatcaccac tgttggtggg gagcccatca 480
ccatcccca gctggagcac ccaaccagc aagacatcga cctgtaccac accatgtaca 540
tggaggccct ggtgaagctc ttcgacaagc acaagaccaa gttcggcctc ccggagactg 600
aggtcctgga ggtgaactga gccagccttc ggggccaatt ccctggagga accagctgca 660
aatcactttt ttgctctgta aatttggaag tgtcatgggt gtctgtgggt tatttaaaag 720
aaattataac aattttgcta aaccattaca atgttaggtc ttttttaaga aggaaaaagt 780
cagtatttca agttctttca cttccagctt gccctgttct aggtggtggc taaatctggg 840
cctaattctg gtggctcagc taacctctct tcttcccttc ctgaagtgac aaaggaaact 900
cagtcttctt ggggaagaag gattgccatt agtgacttgg accagttaga tgattcactt 960
tttgccccta gggatgagag gcgaaagcca cttctcatac aagccccttt attgccacta1020
ccccacgctc gtctagtcct gaaactgcag gaccagtttc tctgccaagg ggaggagttg1080
gagagcacag ttgccccgtt gtgtgagggc agtagtaggc atctggaatg ctccagtttg1140
atctcccttc tgccaccctt acctcaccct tagtcactca tatcgagacc tggactggcc1200
tccaggatga ggatgggggt ggcaatgaca gcctgcaggg gaaagagctt tcgcccgtgg1260
acgattttag ggggggtttc gccaccagtt ggtgtggggg gtta 1304

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(2) INFORMATION ON SEQ ID NO. 22:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 1533 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

095465569 "092000

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

```

gcgaggagct ggcacgcagc cagggccttt gctcaagaag ccataccagc caagaattaa 60
aatctctaaa acatcagtggt atggtgatcc ccactttgtt gtggatttcc cctgagcag 120
actcaccgtg tgcttcaaca ttgatgggca gcccggggac atcctcaggc tggctctga 180
tcacagggac tctggtgtca cagtgaacgg agagttaatt ggggcacccg cccctccaaa 240
tggccacaag aaacagcgca cttacttgcg cactatcacc atcctcatca acaagccaga 300
gagatcttat ctcgagatca caccgagcag agtcatcttg gatggtgggg acagactggt 360
gctcccttgc aaccagagtg tgggtggtgg gagctggggg ctggaggtgt ccgtgtctgc 420
caacgccaat gtcaccgtca ccatccaggg ctccatagcc tttgtcatcc tcatccacct 480
ctacaaaaag ccggcgccct tccagcgaca ccacctgggt ttctacattg ccaacagcga 540
gggcctttcc agcaactgcc acggactgct gggtcagttc ctgaatcagg atgccagact 600
cacagaagac cctgcagggc ccagccagaa cctcactcac cctctgctcc ttcaggtggg 660
agaggggctt gaggccgtcc taacagtga aggccaccaa gtcccagtg tctggaagca 720
aaggaagatt tacaacgggg aagagcagat agactgctgg tttgccagga acaatgccgc 780
caaactgatt gacggggagt acaaggatta cctggcatcc catccatttg acacagggat 840
gacacttggc cagggaatgt ccagggagct ctgaagctgg cagccttaaa gatgcaagt 900
catgaaggac agtgatgtgg ggaggccgtg gggcagctct tttcatggct tgtacacgcc 960
tcagctcctg gcaattagct ggactccatg acccaccctt ggtgcagcat agatccgacg 1020
tctgtctggg cgaagggtag ggggtgggtg gggcggaag cctgagtgc aatgtcattt 1080
ccctctactg cctcttctct cctctcccca ccctgcccac atccacagag gggagagaag 1140
ggcatagctt aaatgcaaca aagtctgtat cttgtcccaa cctgcttttc tgttctgtta 1200
gcatatcata aagtaagcct ttctggtgaa ggaaggttgc tatgaaactt ttttcttgg 1260
tgaaaatggc caagtttagg cactctgctt tttgccttac actaatgctt agaaagctgt 1320
cttttcagtg gtgttgagc cccagatgt gtggccaacc tctgctgcaa aggaatctct 1380
tgctgagtc aggccaccaa tcaggcaaat agccataca tttgatcgtt gtaaaccatg 1440
aagtcttttc ttgcaagacg tttttcttct gctgtggtat cttgccctta aaaattagtt 1500
ttcattaaaa agaaatttga ttgaaaataa aaa

```

(2) INFORMATION ON SEQ ID NO. 23:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

000260 " 5954960

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

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caagtgtgag ccaccacacc tggcctggaa ggaacctctt aaaatcagtt tacgtcttgt 60
at ttgtgttct gtgatggagg aacttgga gaagttgctat tccagtcaat catgtcgagt 120
cactggactc tgaaaatcct attggttcct ttat ttttatt tgagtttaga gttcccttct 180
gggtttgtat tatgtctggc aaatgacctg gggttatcact tttcctccag ggtagatca 240
tagatcttgg aaactcctta gagagcattt tgctcctacc aaggatcaga tactggagcc 300
ccacataata gatttcattt cactctagcc tacatagagc tttctgttgc tgtctcttgc 360
catgcacttg tgcggtgatt acacacttga cagtaccagg agacaaatga cttacagatc 420
ccccgacatg cctcttcccc ttggcaagct cagttgcoct gatagtagca tgtttctgtt 480
tctgatgtac cttttttctc ttcttctttg catcagccaa ttcccagaat ttccccaggc 540
aattttgtaga ggaccttttt ggggtcctat atgagccatg tcctcaaagc ttttaaacct 600
ccttgctctc ctacaatatt cagtacatga ccactgtcat cctagaaggc ttctgaaaag 660
aggggcaaga gccactctgc gccacaaagg ttgggtccat cttctctccg aggttgtgaa 720
agttttcaaa ttgtactaat aggtctggggc cctgacttgg ctgtgggctt tgggaggggt 780
aagctgcttt ctagatctct cccagtgagg catggagggtg tttctgaatt ttgtctacct 840
cacagggatg ttgtgaggct tgaaaaggtc aaaaaatgat ggccccttga gctctttgta 900
agaaaggtag atgaaatata ggatgtaatc tgaaaaaaag ataaaatgtg acttcccctg 960
ctctgtgcag cagtcgggct ggatgctctg tggcctttct tgggtcctca tgccacccca1020
cagctccagg aaccttgaag ccaatctggg ggactttcag atgtttgaca aagaggtagc1080
aggcaaaactt cctgctacac atgccctgaa tgaattgcta aatttcaaag gaaatggacc1140
ctgcttttaa ggatgtacaa aagtatgtct gcatcgatgt ctgtactgta aatttcta1200
ttatcactgt acaaaagaaaa ccccttgcta ttttaattttg tattaagga aaataaagtt1260
ttgtttgtta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1304

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(2) INFORMATION ON SEQ ID NO. 24:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 6945569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

gtccctggcg cctgccttt agccgtgggg ccccccacctc caccctctgg gtttcctagg 60
 aatgtccagc ctccggagacc ttcacaaagc cttgggaggg tgatgagtgc tggtcctgac 120
 aagaggccgc tggggacact gtgctgtttt gtttcgtttc tgtgatctcc cggcacgttt 180
 ggagctggga agaccacact ggtggcagaa tcctaaaatt aaaggaggca ggctcctagt 240
 tgctgaaaagt taaggaaatgt gtaaaacctc cacgtgactg tttggtgcat cttgacctgg 300
 gaagacgcct catgggaacg aacttggaca ggtgttgggt tgaggcctct tctgcaggaa 360
 gtccctgagc tgagacgcaa gttggctggg tggccacac cctggctctc ctgcaggctc 420
 acacaccttc caggcctgtg gcctgcctcc aaagatgtgc aagggcaggc tggctgcacg 480
 gggagagggga agtattttgc cgaaatatga gaactggggc ctctgtctcc caggagctc 540
 cagggccctt ctctcctccc acctggactt ggggggaact gagaaacact ttcctggagc 600
 tgctggcttt tgactttttt tgatggcaga agtgtgacct gagagtccca ccttctcttc 660
 aggaacgtag atgtcggggt gtcttgcctt ggggggcttg gaacctctga aggtggggag 720
 cggaacacct ggcctccttc cccagcactt gcattaccgt ccctgtctct cccagggtgg 780
 gacagtggcc caagcaaggc ctcaactcga gccacttctt caagagctgc ctgcacactg 840
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 ggactttgtc ctggccttcc cttcatggcg tctatgacac ttttgtggtg atggaaagca 960
 tgggacctgt cgtctcagcc tgttggtttc tcctcattgc ctcaaaccct ggggtagggtg 1020
 ggacgggggg tctcgtgccc agatgaaacc atttggaaac tcggcagcag agtttgtccal 1080
 aatgaccctt ttcaggatgt ctcaaagctt gtgccaaagg tcacttttct ttcctgcctt 1140
 ctgctgtgag ccttgagatc ctctcctccag ctcaagggac aggtcctggg tgagggtggg 1200
 agatttagac acctgaaact gggcgtggag agaagagccg ttgctgtttg ttttttggga 1260
 agagctttta aagaatgcat gtttttttcc tggttggaat tgagtaggaa ctgaggctgt 1320
 gcttcaggta tggtaacaat aagtggggga ttttcatgct gaaccattca agcctcccc 1380
 gccggttgca cccacttttg ctggcgtctg ctggagagga tgtctctgtc cgcattcccc 1440
 tgcagctcca ggctcgcgca gttttctctc tctccctgga tgttgagtct catcagaata 1500
 tgtgggtagg ggggtggacgt gcacgggtgc atgattgtgc ttaacttggg tgtatttttc 1560
 gatttgacat ggaaggcctg ttgctttgct cttgagaata gtttctcgtg tccccctcgc 1620
 aggcctcatt ctttgaacat caactctgaa gtttgataca gataggggct tgatagctgt 1680
 ggtccccctt cccctctgac tacctaaaat caatacctaa atacagaagc cttggtctaa 1740
 cacgggactt ttagtttgcg aagggcctag ataggagag aggtaacatg aatctggaca 1800
 gggaggggga tactatagaa aggagaacac tgcctacttt gcaagccagt gacctgcctt 1860
 ttgaggggac attggacggg ggccgggggc gggggttggg tttgagctac agtcatgaac 1920
 ttttgcgctc tactgattcc tccaactctc caccacaaa aataacgggg accaatattt 1980
 ttaactttgc ctattttgtt ttgggtgagt ttccccctc cttattctgt cctgagacca 2040
 cgggcaaagc tcttcatttt gagagagaag aaaaactgtt tggaaccaca ccaatgatat 2100

 ttttctttgt aatacttgaa atttattttt ttattatttt gatagcagat gtgctatttta 2160
 tttattttaat atgtataagg agcctaaaca atagaaagct gtagagattg ggtttcattg 2220
 ttaattgggt tgggagcctc ctatgtgtga cttatgactt ctctgtgttc tgtgtatttg 2280
 tctgaattaa tgacctggga tataaagcta tgctagcttt caaacaggag atgcctttca 2340
 gaaatttgta tattttgcag ttgccagacc aataaaaatac ctggttgaaa tacaaaaaaa 2400
 aaa

2403

000260"6954460

(2) INFORMATION ON SEQ ID NO. 25:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2517 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 6 9594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

cagagtga aa ccttgtgc ct ggtgacaa gtccctccaa agtgctcttc cttctgggtt 60
attcaagcca aatatctggg ttcccccttc tcctcattcc ctagcaaacc ccaattatct 120
tccaagatag gagatatttc ccatccccctt cctttgtaaa tatctcatct ccactggag 180
agcccaggag cctattcctg gcatggatgt tctgtccaca cttgaggctg ggcggtgtat 240
cagacccttc aagcagcctg gctggggccc aggactgagt ctggggtcag ctttcacggt 300
cgcttttccc ttcgtcacca cccaccacag cccaccttgc atgcatggcc agcccctcca 360
ctccagcctg agccatgtgt gcccctgogg gaggacccat tcatgccaga aagctggtaa 420
ctccctccca gcatccctgc ggaaggagtc agtttctgag agtgtgactt ttcaaggcga 480
atgatgggga aggggttcccc agtccccaca gtggccccac ctctggggccc tgcaccagag 540
cccttctgtg tcacggcggg ctgtgcaccc atgcacacac ctacgcacac acaacactcc 600
gcactgcagt atattcttgc caaagatttc ctttaaaagc aagcactttt actaattatt 660
attttgtaaa tgtttatctt cttctgtctt ctcctccctt gaatctattt tactgttgtt 720
tattgttgaa tctgtgtgtc agccaggaga gcgctgtctg gccttgaaca tggcctggga 780
tgggaaaggg tctgggagaa gatgggcaac aaagagccag ggagtcatgg acatcgcac 840
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gtattgtaca ctgacgcgtc cccactcctg tacagctgct ttgtttcttt gcaatgcatt 2460
gtatggcttt ataaatgata aagttaaaga aaactcaaaa aaaaaaaaaa aaaaaaa 2517

```

(2) INFORMATION ON SEQ ID NO. 26:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1668 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

gtatgccctc agaatcacga caactgttgc atgtaacatg gatctgtcta aataccccc 60
ggacacacag acatgcaagt tgcagctgga aactggggct atgatggaaa tgatgtggag 120
ttcacctggc tgagagggaa cgactctgtg cgtggactgg aacacctgcg gcttgctcag 180
tacaccatag agcggtatct caccctagtc accagatcgc agcaggagac aggaaattac 240
actagattgg tcttacagtt tgagcttcgg aggaatgttc tgtatttcat tttggaaacc 300
tacgttcctt ccactttcct ggtgggtgtg tcctggggtt cattttggat ctctctcgat 360
tcagtcctcg caagaacctg cattggggac aacaaaggaa gtagaagaag tcagtattac 420

taatatcatc aacagctcca tctccagctt taaacggaag atcagctttg ccagcattga 480
aatttcacgc gacaacgttg actacagtga cttgacaatg aaaaccagcg acaagttcaa 540
gtttgtcttc cgagaaaaga tgggcaggat tggttgattat ttcacaattc aaaaccccag 600
taatgttgat cactattcca aactactgtt tcctttgatt tttatgctag ccaatgtatt 660
ttactgggca tactacatgt atttttgagt caatgttaaa tttcttgcat gccataggtc 720
ttcaacagga caagataatg atgtaaatgg tatttttaggc caagtgtgca cccacatcca 780
atggtgctac aagtgactga aataatattt gagtctttct gctcaaagaa tgaagctcca 840
accattgttc taagctgtgt agaagtccta gcattatagg atcttgtaat agaaacatca 900
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000260"69545550

(2) INFORMATION ON SEQ ID NO. 28:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

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ctccgagggc aggaacgctc cgtctggaac ggcgcagact tttgccatgg gcttcatgac 60
gggcaccatt tccagtatgt accaaaccaa agccgtcatc attgcaatga tcactactgc 120
ggtaggtatcc atttcagtca ccatcttctg ctttcagacc aaggtggact tcacctcgtg 180
cacaggcctc ttctgtgtcc tgggaattgt gctcctggtg actgggattg tcactagcat 240
tgtgctctac ttccaatacg tttactggct ccacatgctc tatgctgctc tggggggccat 300

ttgtttcacc ctgttccctgg cttacgacac acagctggtc ctggggaacc ggaagcacac 360
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cttcaccttt gtgctgcagc tgatggggga tcgcaattaa ggagcaagcc cccattttca 480
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gaaatcaaat cagcccaagg atatagttag gattaattac ttaatagaga aatcctaact 1680
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aaaaaaaaa gtaaaattaa tttgtgtt

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09545569.092000

(2) INFORMATION ON SEQ ID NO. 29:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3479 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260 "E9994960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

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agaaatgggt ttctacaaag atgcaaagac tgctgcttct ggaattccct accacagcga 180
ggccccgtgt agtttgaaag aagctgtctg cgaagtggcc cttgattaca aaaagaagaa 240
acacgtattc aagctaagac taaatgatgg caatgagtac ctcttccaag ccaaagacaa 300
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gaggcagctg caggaggtatg cagcccgctt ccaggcggcc tatgogggtg acaaggccga 660
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gcacaagctt tgaaaaactac agcaaacagt aataaatgtg actgttttgt agttataaga 3420
gagaaaaaaa agaaaaaaga ggaaaaaaa agaaagaaaa aagaagagga ggagagaac 3479

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(2) INFORMATION ON SEQ ID NO. 30:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 933 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

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gctcctccct tccttctttt tacatttttag tcttagcatt tactttcccc accccacatt 60
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ttcatgaaaag ggctgttaga gctgcctggg aagaaggcgt gccttgggga actgggaaga 180
tgccgtcagt gtgggtgggc aggaggacag ccagtcgtcc tgctgccagc ccaatagctt 240
ccagcggcag gtgcccaggt gctaccggag cccctcatag gggtaggggc agggactgca 300
cctcctccag gcactcatcg taagcctcct ggtactcctc atggggcttg accattatca 360
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gctgtttgga aaaaagctgt acaacctgta tgccaggaag tcaccaactg atgaccacc 480
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acaaagctct ttcacataca tctatctctt tattctcata gtccacagat aactgactat 840
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ccaagaagtg ataatgtagg taccacaagt cca

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(2) INFORMATION ON SEQ ID NO. 31:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2783 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

00260"6954360

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

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gactttaaaa aaattttttac agttattttt attttgtaga atgagctgaa agccagtggg 60
ggcgaaatca aaattcataa aatggagcaa aaggagaatg tgccccagg tcctgagggtc 120
tgcatacccc atcaggaagg ggaaaagatt tctgcaaatg agaatagcct ggagtcctgt 180
tccacccctg ccgaagatga ctcccgtgac tcccagggtta agagtggagg tcaacagcct 240
gtccatccca agccactaag tccagattcc agagcctcca gtctttctga aagttctcct 300
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acagtctatc caatggagcg tctcttgagg aaccagcagg tgtttcacat cagctgcttc 420
cgttgctcct attgcaacaa caaactcagt ctaggaacat atgcatcttt acatggaaga 480
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000260"6954960


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aattaaacca actataggcc tttttcttgg gatgattttc tagtcttaag gtttggggac2520
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ggagagggtgt cttaaagctgt aggcctttct ttgtactgca tttatagaga tttagcttta2640
atatttttta gagatgtaaa acattctgct ttcttagtct tacctagtct gaaacatttt2700
tattcaataa agattttaat taaaatttga aaaaaaagga aaggggaggg ggggtggagg2760
aaaaaaaaa gggcgggccgc cgc                                     2783

```

(2) INFORMATION ON SEQ ID NO. 32:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3411 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

gaagctctgt tgtctcggga acatgtcttg gaattggaga acagcaaggg cccagcctg 60
 gcctcttttag agggggaaga agataagggg aagagcagct catcccaggt ggtggggcca 120
 gtgcaggagg aagagtatgt agcagagaag ttgccaagta ggttcacga gtcggctcac 180
 acagagctgg caaaggacga tgcggcgcca gcacccccag tcgcagacgc caaagcccag 240
 gatagaggtg tcgagggaga actgggcaat gaggagagct tggatagaaa tgaggagggc 300
 ttggatagaa atgaggaggg cttggataga aatgaggaga gcttggatag aaatgaggag 360
 ggcttgata gaaatgagga gattaagcgg gctgccttcc agataatctc ccaagtgatc 420
 tcagaagcaa ccgaacaggt gctggccacc acggttggca aggttgcagg tcgtgtgtgt 480
 caggccagtc agctccaagg gcagaaggaa gagagctgtg tcccagttca ccagaaaact 540
 gtcttggggc cagacactgc ggacctgcca cagcagaggc agctgttgcc ccgccggatg 600
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 gctgcctgaa gagccttctg tccagcccca ccaaggacag taagccaaat atctctgcac 720
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 gtgtcccttt ggtggcttct ccaggacact gctcagattc tttcagcact tcagggcttg 900
 aagactcttg cacagagacc agctcgagcc ccagggacaa ggccatcacc ccgccactgc 960
 cagaaagtac tgtgcccttc agcaatgggg tgetgaaggg ggagttgtca gacttggggg 1020
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 gcatggattc cgtggatagc tgttgcagtc tcaagaagac tgagagcttc caaatgcccl 1140

 aggcaggctc caaccctaag aaggtcgacc tcatcatctg ggagatcgag gtgccaaagc 1200
 acttagtcgg tcggctaatt ggcaagcagg ggcgctatgt gaggtttctg aagcaaacat 1260
 ctggtgccaa gatctacatt tcaaccctgc cttacaccca gacgctccag atctgccaca 1320
 tagaaggctc tcaacatcat gtagacaaag cgctgaactt gattgggaag aagttcaaag 1380
 agctgaacct caccaatate tacgctcccc cattgccttc actggcactg ccttctctgc 1440
 cgatgacatc ctggctcatg ctgcctgatg gcatcacctg ggaggtcatt gtggtcaacc 1500
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 gcagcctcga ccagcagatg tacctctgtt actctcagcc tggaaatccc accttgccc 1620
 cccagtgga aataacggtc atctgtgccg cccctgggtg ggacggggcc tggtgccag 1680
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 agttttcacc ggaagcagat gccgccatga gcgagatgac ggggaatata gcactgctg 1920
 ctcaggtgac aagttacagt ccaactggtc ttccctctgat tcagctgtgg agtgtggtg 1980
 gagatgaagt ggtgttgata aaccggctcc tggtgagcgg aggccttgcc cagtgggtg 2040
 acagctacta cacaagcctt tgacccccat ggtgcttctt gagagtcttt ttttgactg 2100
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 tgatatttaa ccagttttta taaacttcat ttaggtctct aaacacagac tttttaaatt 2580
 gcaactgtaa atatgaaatg gtcacacat ctgacctgg tcagtgggga ggggaactgg 2640
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 caactgtaaa tatgaaatgg tcatcacatc tgaccttgg cagtggggag gggaaactgg 3060
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 tgtgttttaa caaatgtaat attttgtaac agatacactg gagaacaaa ggaactcaa 3180
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 agagactgtg atctgggaac tttttgctgt acaaaaagta actcattgaa ttaacttgca 3360
 gtggtgtgtt tgattctttt ttagactggc ttcagcattg tgcagtttaa a 3411

(i) SEQUENCE CHARACTERISTIC:

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

(2) INFORMATION ON SEQ ID NO. 34:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1236 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```

gtgggccacc cctaatact attgcttctt aaaggtatct tcacctctt cgcttggtac 60
agccctcaca gctcttcaga gcaagcactg gactacaagg gcatggctca caaaagggtta 120
atggatgggg gttacctagc cctggctaata tccccctcca tccccaaact tctctctctt 180
tttgaagaaa aatgctaagg gcagccctgc ctgccccccc catccccccg tgtaaataata 240
cactatcttt gatagcacac atggggcccc catatctctt ggccttggtt ttgatgttga 300
aatcctggcc ttgggagaga tgccctccag gcagacacag ctgtctgggt caggccaagc 360
ccctttgcaa tgcaagccct ttctgggtgt atgaagtccc tctatgtcgt cgttttcacc 420
agcaactggt gactgtccct tcgacacgga cctgctttga gatttcctga cagggaanaag 480
atctctgtcc atttttttcc tgtgcctaac agcataattg ccttttccta tgtaaataat 540
atgatgggtg atcaagacat aagtaaatga gcctttctgc ctacatcag ccctgtgtat 600
aaagccatta ttctctgatg cactgtttgc ccagtaact cactttaaaa cctctctttc 660
cagtgttccc tctctccctc cagggccact gcttgaagaa gaatatgtat gtttctatct 720
tgtatgtctg tgtgccccct ctgccccgaa agtgctgact atgggggaaat cttttagctg 780
ctgtttttag actccaagga gtggaaatta tgttgaagaa gcaaacctga tacaatttgc 840
ccaaggtaaa cagtttgaaa agacaaatgg gcctgccaaa ctgtacagtt tcttccccaa 900
gagctgttag gtatcaaaat gttgtccttt cccccctccg tgcttttctg gttgagatca 960
tgtcattgat gaactgccaa agtcaggagg ggagggcaga gacttttgtt ttacatctgc 1020
atctctacat gtttttagaca gagacaattt aaggcctgca ctcttatttc actaaagaaa 1080
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agatcaaatg tgaaataaat atgaatggag tggctctctt gtctgttatc tgagttttcal 1200
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000260"69594960

(2) INFORMATION ON SEQ ID NO. 35:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 749 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

```

ggagatgcag aggtaaaagt gtgagcagtg agtttacttt tcaaggcatc ttagcttcta 60
ttatagccac atccctttga aacaagataa ctgagaattht aaaaataaaa aaatacataa 120
gaccataaca gccaacaggt ggcaggacca ggactatagc ccaggctctc tgatacccag 180
agcattacgt gagccaggta atgagggact ggaaccaggg agaccgagcg ctttctggaa 240
aagaggagtt tggaggtaga gtttgaagga ggtgagggat gtgaattgcc tgcagagaga 300
agcctgtttt gttggaaggt ttggtgtgtg gagatgcaga ggtaaaagtg tgagcagtga 360
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tgaagggtaa agaagtttga tattaaagga gttaagagta gcaagttcta gagaagaggc 480
tgggtgctgtg gccagggtga gagctgctct ggaaaatgtg acccagatcc tcacaaccac 540
ctaatacaggc tgaggtgtct taagcctttt gctcacaaaa cctggcaca tggctaattc 600
ccagagtgtg aaacttccta agtataaatg gttgtctgtt tttgtaactt aaaaaaaaaa 660
aaaaaagttt ggccgggtgc ggtggctcac gcctgtaatc ccagcacttt gggaggccaa 720
ggtgggggga tcacaaggta actagatgg

```

(2) INFORMATION ON SEQ ID NO. 36:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

09546569 " 092000

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

```

gtgaccccca taggcctgag gcttgtgcag gcagtgggcg tggggtaagg cttcctgatg 60
ccccctgtcc ctgcccagaa cctgatggcc ctcattagtc cttggctctt atcttggaag 120
cacaggcgct gacagccgtc ccagcccttc tgtctgcggg cctgaaccaa acggtgccat 180
ggggaactgt ctgcacaggg cggagtctcc ccctcaactg agaactcaag tcagctggac 240
ttcgaagatg tatggaattc ttcctatggt gtgaatgatt ccttcccaga tggagactat 300
gatgccaaac tggaagcagc tgccccctgc cactcctgta acctgctgga tgactctgca 360
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atgcttttca gacctctctt ccgctggcag ctctgccctg gctggcctgt cctggcacag 480
ctggctgtgg gcagtgcctt cttcagcatt gtgggtgccc tcttgcccc agggctaggt 540
agcactcgca gctctgcctt gtgtagcctg ggctactgtg tctggtatgg ctcagccttt 600
gccaggcctt tgctgctagg gtgccatgcc tccctggggc acagactggg tgcaggccag 660

gtcccaggcc tcacctggg gctcactgtg ggaatttggg gagtggctgc cctactgaca 720
ctgcctgtca ccctggccag tgggtgcttct ggtggactct gcacctgat atacagcacg 780
gagctgaagg ctttgcaggc cacacacact gtagcctgtc ttgccatctt tgtcttggtg 840
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ctgctcctcg ccctattctg ccaccaggcc acccgacccc tcttgccctc tctgcccctc 1140
cctgaaggat ggtcttctca tctggacacc cttggaagca aatcctagtt ctttcccac 1200
ctgtcaacct gaattaaagt ctacactgcc tttgtgaaaa aaaaaaaaaa a 1251

```

(2) INFORMATION ON SEQ ID NO. 37:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 3283 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

000260" 6554550

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

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ctggcctcag caccttccag aactgggttac ctagtaccce cgccacctcc tgggggtggac 60
tcaccagttc caggaccaca gacaatggtg gggagcagac tgccctgagc ccccaagagg 120
ccccgttctc tggcatctcc acgcccccg atgtgctcag tgtaggcccg gagcctgcct 180
gggaagccgc agccactacc aagggccttg cgactgacgt ggcgacgttc acccaagggg 240
ccgccccagg cagggaggac acggggcttt tgaccaccac acacggcccc gaagaagccc 300
cacgcttggc aatgctgcag aatgagttgg aggggctggg ggacatcttc caccatga 360
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aacaggggag ctacttcgtt cgtttaggtg acctgggtcc cagcttccgc cagcgggcat 480
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cagagcggct ggtgcagagc cgcgagggtg tgcaccaggc ttggcagggg ttagagcagc 900
tgctggaggg cctacagcac aatcccccg ctagctggct ggtagggccc ttcgccttgc 960

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000260"69594960

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 gccctagacc tttggggctg cagctggctg agcgccgagg ggctgcggag gcagtgacct1140
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 aagggcattt gtttgccccg ctagcaaccc ttttatatct agcagggtct tccagtcct1380
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 taagaaccac attccctcat agtagaaagt actagaaaaa gcgacactgc catcatcatc1560
 ccaaggcagg ctgctactgc ctttgctgac ccccggggtg gcctcacggt ggggacaaag1620
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 ggatcagac agggctggga acagccacag aggtgcgtg cctatggcac agcccttct1920
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 cccactgcac cagcaatgct agaaaaccaa gccataaaaa gtgatttctt ttttcattaa3240
 aaaaaagaaa aaaagagaca gaggaagtag atgctggccg gcc 3283

(2) INFORMATION ON SEQ ID NO. 38:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

gaggggagaa ggaaggagg

2720

(2) INFORMATION ON SEQ ID NO. 39:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

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gccggccgcc ctttttaacc cccttccctt cctttttttc tgttgctgaa tgatatttta 60
ttagcttgat aatttgggcc tgcccttagc attaataagc ttcagcacta gtcacaagac 120
tttcattcac tgggtggggaa actttcttgt tttaaaaaat gcaattcaag aaagggcatc 180
tatttcttgg gggctgcggt gacagcaggc ttctcttcac ggggtgatggg aatgggtgcgc 240
tcagggccag agacctgttt ccttggtcca ttcacagtga ggaccccatc agatgacagg 300
gatgaagtaa tggtgagagg gtctacatca gctgggateg ggtatttcct gtggaactcc 360
ctggagatga aaccatgttc atcctggcgc tcttcagtgt ttccatgcac ctcaatcaca 420
tctcccaaca ccttaacttt gagttcctct ggggagaagt gcttcacatc caggttgaca 480
gagaacctgt ccttctccag gcgcctctct gagagtccag tgtcaaacca gctgggtgcc 540
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tcagactcca acaggtgctc tccgaagaac tgggtcaaaga ggcggctggg ggagtggaaa 660
ggaaagaagg ggcggcggat ccaggggtgg tggatggcga tgtccatggt ggctaggtga 720
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atatgcagtc ttgtgaagct tctggaatgg tgatgtcagg ggttttatta tcctagctca 840
ccagcagttc atggagactt gtgatccggg atttggaat gtgacacata cccagtactc 900
actgagctaa gaaaagagag acacaaacac gtctgagccg gccagtgact tgtcatggtc 960
ttgtttcact agctttctgt ccacacccaa tggcacccac cccacccctt gttctctgaa 1020
gctggtacag agtcag                                     1036

```

(2) INFORMATION ON SEQ ID NO. 40:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2659 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

00646569 "092000

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

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accacacggg ctgccctccc ctgcgcactc ccctcgctgc ccgggccccg agcgagctgg 60
ggccgcacag attcacaatg ttgaaagccc ttttcctaac tatgctgact ctggcgctgg 120
tcaagtcaca ggacaccgaa gaaaccatca cgtacacgca atgcactgac ggatattgag 180
gggatcctgt gagacagcaa tgcaaagata ttgatgaatg tgacattgtc ccagacgctt 240
gtaaagggtg aatgaagtgt gtcaaccact atggaggata cctctgcctt ccgaaaacag 300
cccagattat tgtcaataat gaacagcctc agcaggaaac acaaccagca gaaggaacct 360
caggggcaac caccgggggt gttagctgcc gcagcatggc aaccagtga gtgtgccc 420
ggggtggttt tgtggccagt gctgctgcag tcgcaggccc tgaaatgcag actggccgaa 480
ataactttgt catccggcgg aaccagctg accctcagcg cattccctcc aacccttccc 540
accgtatcca gtgtgcagca ggctacgagc aaagtgaaca caacgtgtgc caagacatag 600
acgagtgcac tgcagggacg cacaactgta gagcagacca agtgtgcatc aatttacggg 660
gatcctttgc atgtcagctg cctcctggat atcagaagcg aggggagcag tgcgtagaca 720
tagatgaatg taccatccct ccatattgcc accaaagatg cgtgaatata ccaggctcat 780
tttattgcca gtgcagtcct gggtttcaat tggcagcaaa caactatacc tgcgtagata 840
taaataaatg tgatgccagc aatcaatgtg ctacagcagt ctacaacatt cttggttcat 900
tcctctgtca gtgcaatcaa ggatattgag taagcagtga caggctcaac tgtgaagaca 960
ttgatgaatg cagaacctca agctacctgt gtcaatatca atgtgtcaat gaacctggga1020
aattctcatg tatgtgcccc cagggatacc aagtggtagg aagtagaaca tgtcaagata1080
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acaaatacat gagcatccga tctgataggt ctgtgccatc agacatcttc cagatacagg1320
ccacaactat ttatgccaac accatcaata cttttcggat taaatctgga aatgaaaatg1380
gagagtctta cctacgacaa acaagtccct taagtgaat gcttgtgctc gtgaagtcac1440
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cttttctaag agteaaccac aggcatttaa gtcagccaaa gaatatgttt accttaaagc1620
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aattcaaaca attacacat ggtataaagt gggcatttaa tatgtaaaga ttcaaagttt1740
gtctttatta ctatatgtaa attagacatt aatccactaa actggtcttc ttcaagagag1800
ctaagtatac actatctggt gaaacttgga ttctttccta taaaagtggg accaagcaat1860
gatgatcttc tgtggtgctt aaggaaactt actagagctc cactaacagt ctcataagg1920
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gattgtgaat attttgtaaa aaacagtaag caaaattttc cagaattccc aaaatgaacc2220
agatatcccc tagaaaatta tactattgag aaatctatgg ggaggatatg agaaaataaa2280
ttccttctaa accacattgg aactgacctg aagaagcaaa ctcggaataa ataataacat2340
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ttctcatctt cgtacttgat gctcacagag gaagaaaatg atgatggttt ttattcctgg2520
catccagagt gacagtgaac ttaagcaaat taccctccta cccaattcta tgggaatattt2580
tatacgtctc cttgttttaa atgtcactgc tttactttga tgtatcatat ttttaataaa2640
aaataaatat tcctttaga

```

2659

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 41:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2939 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000250"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

tttttttttt	ttttttttgt	ggttaataaaa	tgttgtcaat	tttattaaaa	gctgattcca	60
ttttttcaca	cagttaagta	cgtttctttc	ttgttttggt	aaagcccatt	tcataagagt	120
gagttggctc	tgtgagacca	tcactgataa	agacacatac	agttagcacc	acacatttat	180
aaatgcagat	agccacaatg	acctttccaa	tatgtacaag	ctccattttac	acatccacac	240
atgtattttac	agctaataaa	taaaatgtaa	agccagaaca	tccttgatat	atataacaaa	300
gttttttcgga	gccagagttc	ccagtgctat	gtgctgcttt	agtgaattctt	ttaagttaat	360
gcacctgtgg	tcacaaccca	aatccagaaa	ttaatatgaat	taataaaggg	gatgccaaca	420
acaaatcata	catcatttta	tttttagaga	gaattcattc	caagcctgat	gatgttaatc	480
acaacattgg	tcctactatt	tataggcacg	atcatctctc	tcagagaaaag	ggcgaagtt	540
ctggcacatc	aggaacaatt	tctactccga	catgttccaa	tacatccctt	gatcgactgt	600
tttcccttcc	gaattatgct	gaaggacaac	acacatgcag	agctttctag	tatgtgttca	660
gatatcacat	actttcacag	tcgggttccc	agctatagcc	tctgagatat	ttgacatctt	720
tatcatttca	tattttatacg	tagaagagca	ttctgaaaaa	taggagatct	agttttataaa	780
tagttgttgc	ctcactcttg	attagttggt	aaaaacaaca	aatagcaacc	ctcatggtaa	840
tcctcttggc	tcattgcacg	cgatggttta	caagcactgc	ttaggaattcc	acctccagaa	900
cctctccacc	ctttttactta	gtaaaaacgg	tccttgtcta	aaatctgtag	aagctcacac	960
aatgcaaaat	ttgaactcaa	acctattctt	tcatgtcaaa	gccaggaaca	aaagagacgc	1020

actggaagta	caactgaagc	atgaccaagc	taagcctaaa	actgaagagt	aactgtcagal1080
tattgaatga	ttttaaattg	atgaaaatca	tttggagaat	ctaataataa	aattacggtt1140
tctttttttt	tttctgcacc	attcaaatta	tgtgtcagct	gaggattaca	ggctcatttt1200
caacacctac	ccagagaaca	ttattataat	ataatcttga	gacaaaaaag	aagggggagal260
gagggtattaa	gcaataaacg	ataaagccta	ttaagaatta	attgatctag	attttatatc1320
tccgtgaatt	tgtaaacttg	tcatgatgca	ggccaatggt	agggactggt	taaaacctct1380
gtgtttatca	gaccttttct	tcgtccctct	ccaagttaca	tgttcctggt	tgacgtctgg1440
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tgagaaggcc	tcagtcggaa	agatccagaa	ttccaattaa	aataggaggt	tctaaccaat1620
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cactcttcca	tttgagcttc	aacatgagta	gttctccaat	atctacctct	gtgtaaatta2220
ggaaggaagta	ggtcttattt	gtggaacctt	caggcagagt	gaatgggatg	ttctcactct2280
cgccgcacggt	gccatacaga	gaaatctcaa	aggcctgatt	ggtatgggtt	tcactctcag2340
tcccagaaaa	atgaatcttt	acttggtaat	ggaagacttt	gtagggcata	tgagaacagat2400
tcttcaggta	cattttgctg	cttcttttgg	ctctgacttt	attggtctca	tgagccagat2460
tgttcagcgc	gttcttttcta	caactcaagc	agagcccttt	ctcaaaggct	tccttggaac2520
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tggagcgctc	gtgggagcac	ttcactagct	ggtccacatc	tccaagtcct	ctctctgcaa2640
tcacgcggat	agctcttcca	atgtttacatc	ctggctgaaa	agtacctoca	ttcgggtaaa2700
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catactcaaa	gttaggtcca	gctggatcga	ggccagtaat	tctgttgaaac	ttctttattg2880
gtcagacttc	ctgcaatgcc	agcagcatgg	gctccaaggc	tgtatcccaa	gaatggac 2939

(2) INFORMATION ON SEQ ID NO. 42:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3670 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

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gcatcgccat gacgcccgcc aatgccaccg aagcctccaa gcccgaaggc acaacgggtgt 60
gtcctccctg tgacaacgag ttgaaatctg aggccatcat tgaacatctc tgtgccagcg 120
agtttgcact gaggatgaaa ataaaagaag tgaaaaaaga aaatggcgac aagaagattg 180
tccccaagaa gaagaagccc ctgaagttgg ggcccatcaa gaagaaggac ctgaagaagc 240
ttgtgctgta cctgaagaat ggggctgact gtccctgcca ccagctggac aacctcagcc 300
accacttctt catcatgggc cgcaagggtga agagccagta cttgctgacg gccatccaca 360
agtgggacaa gaaaaacaag gagttcaaaa acttcatgaa gaaaatgaaa aacctagagt 420
gcccacactt tcagtcctgtg ttttaagtgt tctcccgggg gcaggggtggg gagggagcct 480
cgggtggggg gggagcgggg gggacagtgc cccgggaacc cgggtgggtca cacacacgca 540
ctgcgcctgt cagtagtgga cattgtaatc cagtcggctt gttcttgcag cattcccgt 600
ccctccctc catagccacg ctccaaaccc cagggtagcc atggccgggt aaagcaaggg 660
ccatttagat taggaagggt ttttaagatcc gcaatgtgga gcagcagcca ctgcacagga 720
ggaggtgaca aaccatttcc aacagcaaca cagccactaa aacacaaaaa gggggattgg 780
gcggaaagtg agagccagca gcaaaaaacta cattttgcaa cttgttggtg tggatctatt 840
ggctgatcta tgcctttcaa ctgaaaaatt ctaatgattg gcaagtcacg ttgttttcag 900
gtccagagta gtttctttct gtctgcttta aatggaaaca gactcatacc acacttaca 960
ttaagggtcaa gcccagaaag tgataagtgc agggaggaaa agtgcaagtc cattatgtaa1020
tagtgacagc aaagggacca ggggagaggc attgccttct ctgcccacag tctttccgtg1080
tgattgtctt tgaatctgaa tcagccagtc tcagatgcc caaagtttcg gttcctatgall140
gcccggggca tgatctgatc cccaagacat gtggaggggc agcctgtgcc tgcctttgtg1200

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09646569.092000

tcagaaaaag gaaaccacag tgagcctgag agagacggcg attttcgggc tgagaaggca1260
 gtagttttca aaacacatag ttaaaaaaga aacaaatgaa aaaaatttta gaacagtcca1320
 gcaaattgct agtcagggtg aattgtgaaa ttgggtgaa agcttaggat tctaattctca1380
 tgttttttcc ttttcacatt tttaaaagaa caatgacaaa caccactta tttttcaagg1440
 ttttaaaaca gtctacattg agcatttgaa aggtgtgcta gaacaaggtc tcctgatccg1500
 tccgaggctg cttcccagag gagcagctct ccccaggcat ttgccaaggg aggcggattt1560
 cccgtgtagt gtagctgtgt ggctttcctt cctgaagagt ccgtggttgc cctagaacct1620
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 tcctttgaac ttgattgcct atggatcaaa gaaattcaga acagcctgcc tgtccccccg1740
 cactttttac atatatttgt ttcatttctg cagatggaaa gttgacatgg gtggggtgtc1800
 cccatccagc gagagagttt caaaagcaaa acatctctgc agtttttccc aagtaacctg1860
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 ggggccctag cctgacccgg aggaaaggat ggtagattct gtttaactct gaagactcca2160
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 gcacagagct gcactatcac gagcctttgt ttttctccac aaagtatcta acaaaaccaa2880
 tgtgcagact gattggcctg gtcattgggt tccgagagag gaggtttgcc tgtgatttcc2940
 taattatcgc tagggccaag gtgggatttg taaagcttta caataatcat tctggataga3000
 gtcttgggag gtccttggca gaactcagtt aaatctttga agaataattg tagttatctt3060
 agaagatagc atgggaggtg aggattccaa aaacatttta tttttaaaat atcctgtgta3120
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 agagctccag tttgcatttg gatgtgtaaa ttacagtaat cccatttccc aaacctaaaa3240
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 tgtgaaaatg ttttacattc catttcattt gtgttgtttt ttttaactgca ttttaccaga3540
 tgttttgarg ttatcgctta tgtaaatagt aattcccgtg cgtgttcatt ttattttcat3600
 gctttttcag ccattgtatca atattcactt gactaaaatc actcaattaa tcaataaaaa3660
 aaaaaaaaaa

3670

09646569.092000

(2) INFORMATION ON SEQ ID NO. 43:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1025 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

```

ctttaaccag ttatttacag tgtgctcatt cgttcagaaa ttagatacaa aatctcaaga 60
cctgttacta ctgattttat taaatcagag tctttaattc ttgcatgttt gtatctaatt 120
tctgaacgaa tgagcacact ttaaccagtt atttacagtt acctttttcc ttttaaccgga 180
ttgtgaaagc ttcattgtatt ttaatttaga ttctgtgttt ttaagggttc tgagcatgaa 240
gctggcagat agtcggcagg actcattttt tcatcatggc tggctgattt ctccatagat 300
tgataacagt attttgttat cttgcttctc tgtagttttg catcagctgt ttaactttga 360
gctgagttag gggagagggg taaagagaaa gaaacttaag ttttctttca cagaactcca 420
ccattgtggg ctttgagaga gccctaaagc attgtacctt gtggtacctt gtgacttcca 480
accaaagcct ttgagtatgc actaaatagg tgagaagaaa ggagagaagg tttttagggt 540
agaaaccttt aaccgataga aggatatggt atgttgtaaa gctggaacca agtttgcatt 600
tttgagggct tgagatgaag ggaagactct taccagatag taagacagct gagttttcct 660
cagttttctc gtcttaacac tagtggacaa ttctagcatt ttgtttggag gatttcagag 720
ttaacctcat ggaattcagg attttttagc aagtttgctt ttggttttat cttggctttt 780
agtaatcatg ttggctggtc tggtcacagg tgactgtgaa acagatgcc tggctctgct 840
ttcatcactc taggatcatg aagtgcctat ctatttcctg gttatgaata ttaagggttg 900
aattacattt ttattgattg tttggatcag agctcagttc ctgtagaaaa cgaactgtaa 960
aagaccatgc aagaggcaaa ataaaacttg aagtgaatgc taaaaaaaaa aaaaaaaaaa 1020
aaaaa                                           1025

```

(2) INFORMATION ON SEQ ID NO. 45:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 538 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

000260 " 6954960

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

```
ccaggaggct gtaggggga gaatgttctt ttggccactg tgaagcctca ggaaggggct 60
cggattgctc aaggacccat gggagagagg aggccttgac tgggctgcct gcctgtgagg 120
tctctggact agaggtccaa cgcagtccag ctgacaagga tggaatacgc catgaagtcc 180
cttagccttc tctaccccaa gtccctctcc aggcattgtg cagtgcgtac ctctgtggtg 240
accagcagc tgetgtcgga gccagcccc aaggccccc gggcccggcc ctgccgcgta 300
agcacggcgg atcgaagcgt gaggaagggc atcatggctt acagtcttga ggacctcctc 360
ctcaaggctc gggacactct gatgctggca gacaagccct tcttcctggg gctggaggaa 420
gatggcacia ctgtagagac agaagagtac ttccaagccc tggcagggga tacagtgttc 480
atggtcctcc agaaggggca gaaatggcag ccccatcag aacaggggac aaggcacc 538
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(2) INFORMATION ON SEQ ID NO. 47:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 360 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

000260"6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

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gccacggggtc cggccacggg tgccggccacg ggtccgacaa tagtatgcag ctaaaaaata 60
attgtatgtc tttatatact aatatgtaat aatcttcagg tgaaaaaggc aagccacaga 120
aatgtgtata gcgcacttcc catttgtgtt tcagaaagga gtagaatata aacacataat 180
tgcttatgta tgcttattca gaataaatgg gtaacactga ttacttttgg gaggggaacc 240
agtaggttga ggacaggaga gggaagggtc ttaacactta cacccttttg tacattttga 300
atthtgaacc atgtgactgt attacctatt caaaataaac aataaatggg cccaaacagg 360

```

(2) INFORMATION ON SEQ ID NO. 48:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2192 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000250" 69994960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

gagcgctgcg	cccacacct	ctctgtcca	gacctgccc	gctgggcag	ggccgggcgc	60
cgctcggtga	tgagccacag	aacctcttcc	accttccgag	cggagagaag	tttccattcc	120
tcttctctt	ctctctcgc	tgccacctcc	tctcggcct	cccggtctct	ccgggccag	180
gaccgccca	tggagaaggc	cctgagcatg	ttttccgatg	actttggcag	cttcattgcg	240
cccactcgg	agcccttggc	cttcccagcc	cgcccgggtg	gggcaggcaa	catcaagacc	300
ctaggagacg	cctatgagtt	tgcggtggac	gtgagagact	tctcacctga	agacatcatt	360
gtcaccacct	ccaacaacca	catcgagggtg	cgggctgaga	agctggcggc	tgacggcacc	420
gtcatgaaca	cccttcgtca	caagtgccag	ctgcgggagg	acgtggaccc	gacgtcggtg	480
acctcggtc	tggggaggga	cggcagcttc	actatccggg	cacggcgcca	cccgcataca	540
gaacacgtcc	agcagacctt	ccggacggag	atcaaaatct	gagtgctct	cccttccctt	600
tccctgtgcc	ccccgcccc	cgctgccag	caaagcctcg	ctaaccctat	tacaacagct	660
ccaggacatc	tcagcccagg	ttctagcccc	cacgcacccc	agaccccagg	tgaccatcc	720
tcccaaacta	gggcctcca	ctctatccag	ggcaggccag	ggactccctg	gcctgacaca	780
tgatgccccag	atttcagatt	tggcctcctg	cacttaatcc	agagtacagg	ggctggggtc	840
agggaaaggaa	gatctaaaga	acctactgtg	ggtcaggggga	atgggaccag	caggacatat	900
gggcaagctc	tgcaggacag	acaggcagac	aaacctctcg	atctatgaag	tctctgcagg	960
gcaaggggac	cagggaacctg	gaacctctct	ggccaagggg	agtgggagag	acagagggaal	1020
ggtcacaggc	aagggtgcct	atctaagtgg	aactaattgc	ccgagggtc	agcaaggccal	1080
agaggagaca	gccgtgcagg	taaaactccc	ctctaccagc	ctccaaggcc	cacgcagcgil	1140
agcaggctgc	ctgccccacc	cgtgccccca	gccagctggc	tgtgccaggg	cagagccatg	1200
ccacatctgt	atatagatgg	ggtttttcca	atacagctgg	ttcgtgataa	actgcatgaal	1260
actcctgccg	tcttgcgcct	gctggggcct	ccaggcaagg	ccacgtgggg	ttgggggtgg	1320
ggctggtcct	tctccctccc	acaggcctgt	gttcttgggg	ctgctcccat	gcagacaggal	1380
tcaccttaaca	gagatggaag	ccaggggcatg	gatggggcct	tgggtcctcg	aggttggacc	1440
ccagcttctt	gccaccttcc	cctccggggca	gtcagctctc	catccatccc	cctctttaat	1500
ctatgaatct	ataggctcgg	tgtgtgtaac	acacacaccc	ctatcgttgt	ccttcaaata	1560
ctcagcatta	ccattgggtg	agggcaaat	cagagctttc	tcaaatcaga	tttacaatct	1620
ccattttcat	taacggggaa	acatcccga	gccactgagt	gtgtgcttt	gtcactgaag	1680
gttagatctg	aaccagggtt	gtcaacagct	gctctcaact	ccccacctct	gggcactgag	1740
gagratcttc	cctcattcta	cctctctaag	gctatgcacc	cctccccacg	tcttcagct	1800
gggggatggg	gggagtcata	ggaaaagccc	ccatctccca	tctgggatag	ggaccttcca	1860
tcagccttaa	ccctgggaaa	tgccgtctgc	cccagtgac	tcttggttc	gtctcccaca	1920
tacagaagca	gggtggaggg	gaagggtggg	tctcagttag	caggggtccc	cagggcaagt	1980
cagcctcttc	ccctcatggc	tctctggtca	gtgtgcctta	gggtggcctc	tcactcccac	2040
cactctgggc	cccttggggc	aggactgggg	agggggcgtg	gggagagccc	tgacgctgga	2100
acctgtatac	acaataaagg	acagctctac	agacaaaaag	aggccgcctg	ccggagtctt	2160
caaacttagg	gcagggcctt	acttgagaga	aa			2192

(2) INFORMATION ON SEQ ID NO. 49:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2952 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

```

gtgCGGatgc cggccggcag cagcatcatg gctcacgggc cggcgcgct gatgctcaag 60
tgcgtgggtgg tcggcgacgg ggcgggtgggc aagacgtgcc tactcatgag ctatgccaac 120
gacgccttcc cggaggagta cgtgccacc gtcttcgacc actacgcagt cagcgtcacc 180
gtggggggca agcagtacct cctaggactc tatgacacgg ccggacagga agactatgac 240
cgtctgaggc ctttatctta cccaatgacc gatgtcttcc ttatatgctt ctcggtggtta 300
aatccagcct catttcaaaa tgtgaaagag gagtgggtac cggaacttaa ggaatacgca 360
ccaaatgtac cctttttatt aataggaact cagattgac tcgagatga ccccaaaact 420
ttagcaagac tgaatgatat gaaagaaaaa cctatatgtg tggaacaagg acagaaacta 480
gcaaaagaga taggagcatg ctgctatgtg gaatgttcag ctttaaccca gaagggattg 540
aagactgttt ttgatgaggc tatcatagcc attttaactc caaagaaaca cactgtaaaa 600
aaaagaatag gatcaagatg tataaactgt tgtttaatta cgtgagaaac atcttcagt 660
gccaaggaaa ctgtccattt ctctcagaaa gcaaatgaaa tgctacagct ataccagac 720
cttttatagg taatgaagca gttcaaaact tgaaagaaaa caaacctgt cctcagaatt 780
ctataaagtg tattaagaat gttccttaaa ggtttaagaa gcagtaagca gcatctgaag 840
ccacaatcta ttataaatatc tttatttcaa ctagaaggta caatctctca ggggtttcat 900
agttaaaaaa gctacaatca catcatgttg taactacgta aaaaacagag ctgtaaatgg 960
aactgcttgg ctttgaccat acacatttct gccagccct tacagaatct gcacaaagaa 1020
atatctccct ttgctccagt taattgttct tgtatgtaag ttgctttcta ttccagtata 1080
tcagagtggt tgaaataaca aggccagcca cgtagccaaa ggtcgctcca agcgtacagg 1140
agatgggcca tacttgagga gagaatgtat gagatcaaaa aagaacaaat gttttattat 1200
tacttgagca caagtgtaac ctaaatattt ctatatataa gcttaatgtg ctttcttaaa 1260
gaatgccaaa agtgtataaa ggtcataact gcatttatca tgaacactaa aaatgtacac 1320
attttagtta atgtgcatta aactgtaaca aggttcttgg caattgtaga tttagttgag 1380
cgctccccaa agtgcagtag acacatgcta aaattacaaa taaaattttt gggtcagact 1440
ttgccataat gatagactca atttagctct ctgaactagt tggtaatttt ttttttttaa 1500
ttcccacttt ggctgtgtac atcaaatgaa atgagaagtg tgtatgctga ccaaaccaca 1560
agaaactttc ttaagtgtgt gttaaagagg aaagacctag aatccaagcg tgttacatga 1620
aaattgtaac agagcagctg ctccacctt tcagatatag atgttgaac cacagcagaa 1680
gttatagagc gacaacttat atacacacct agaagtgaag ttaaacaaaa taccggcttc 1740
cagagacccc ttttctccag ccatattaca tcaggctaga agtaattaat gttgatttat 1800
ttcatctaca agcagttggt cctaagtga aaggctctgc ttgaaaaaaa aaagaaaaaa 1860
aagttggagg aaaattttca tgttcttctg tgaagcttat ttggtacact ggagccattt 1920
ctaactttc tctgggggga acaggccaca gaactgtgtt agaggtgaac catcttaatt 1980
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gaacaaccta atgcatttta gagaaacaat ctcatcacat ttttcttagc ctttcttaca 2160
tttaaacttg ctgttgccca aattataatt tttaaatgt ctttggtggg cttctgttaa 2220
ttcacatgac ttgagcttat agctatgtct actgcacaga ttgggtaatg gaacactaaa 2280
cttttatact tgaaaatgac agccttaaat gctcatatca gtcacaaatc taggatgtac 2340
tgtcttggtg tatgtgagct ttgtagagat ttttaaaaaa ataagcatca ccttccattt 2400
gaagagtggg gagagtctac tggatgactg gccaggaact ttctctctga atcgacatt 2460
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tgctcaaatg gaactttatg taactttctt atttaatttt ggtctgctta tttttagata 2580
aaattgaaag gaattgtata aatcaattaa catattagct gagttgtcca acacatggta 2640
taaacgaatt acaacagtaa actattacac atttccaact tgcctttggg gatttatgag 2700
gatttttttt ggtgggggga gggggctcca attcatatct ctgaaacctt tcacacttgg 2760
tttactaatt caaagttaga agtctagaat ttgccctgcc ctaacagaaa cagatttagga 2820
atgtgtctac acaaactggg gtcacctgtt tcttgactgg gatttggttt cctcattata 2880
aatatgggag gtagaacaga gatctccaac gtctctccca tttatcacag taattttctt 2940
attcacagta at

```

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 50:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 615 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

```

gcaaggatgg tctcaatctc gacctcgtga tccgccacc ttggcctccc aaagtgttgg 60
gattacaggc gtgactcacc atgccagcc acttagtttt ttcttattcc cacctttcta 120
tcccatagaa cactcttttt tatcttcctt gaaccatatt gatgagataa atagggctgg 180
gggctggggc ccgctgggtca ctcaacagag tatttccttt ggccgagatg gaagttttgt 240
cccaatagat gagctgctga gtatcaacaa ggtgacattt ttctgctgcc catttgtgtc 300
ctggagacgg tggtagcctg aaggcagagg ccagctgccg caagacagca atgacagtcc 360
acctgccgac ctgattcctg catcatggaa taaccacatg gctaccttct atcctctgtt 420
cccaaattggt ggtggcactt atcctgaagt cgtcaatgat ttccctttga aactacttta 480
ttttactaat ttaaaactatt ttgtactgat gtagccctga ggtagttcat gaaaatgctg 540
tgcactcatt ccatggaata aatgttgga agctgatctt ttctgatata aaatgttgaa 600
tgataaaaaa aaaaaa 615

```

(2) INFORMATION ON SEQ ID NO. 51:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1488 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

000260" 59534550

(vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

```

ttttactgac cttgctagaa gtttacagca aggaagtgcg ggaacatttc acaaatctac 60
aatctgtgag tatcacatcc tgtatagctg taaacactgg aataaggaag ggctgatgac 120
tttcagaaga tgaaggtaag tagaaaccgt tgatgggact gagaaaccag agttaaacc 180
tctttggagc ttctgaggac tcagctggaa ccaacgggca cagttggcaa caccatcatg 240
acatcacaac ctgttcccaa tgagaccatc atagtgtctc catcaaagt catcaacttc 300
tccaagcag agaaacccga acccaccaac caggggcagg atagcctgaa gaaacatcta 360
cacgcagaaa tcaaagttat tgggactatc cagatcttgt gtggcatgat ggtattgagc 420
ttgggggatca ttttggcatc tgettccttc tctccaaatt ttaccaagt gacttctaca 480
ctgttgaact ctgcttacc attcatagga cctttttttt ttatcatctc tggctctcta 540
tcaatcgcca cagagaaaag gttaaccaag cttttggtgc atagcagcct ggttggaagc 600
attctgagtg ctctgtctgc cctggtgggt ttcattatcc tgtctgtcaa acaggccacc 660
ttaaactctg cctcactgca gtgtgagttg gacaaaaata atataccaac aagaagttat 720
gtttcttact tttatcatga ttcactttat accacggact gctatacagc caaagccagt 780
ctggctggaa ctctctctct gatgctgatt tgcactctgc tgggaattctg cctagctgtg 840
ctcactgctg tgetgcggtg gaaacaggct tactctgact tccctggggg gagtgtgctg 900
gccggcttca cttaaccttg cctagtgtat cttatccctg cactgtgttg agtatgtcac 960
caagagtggg agaaggaaca accagccaat cacgagatac acatgggagg gcatttgcac 1020
tgtgatggaa gacagagaag aaaagcagat ggcaattgag tagctgataa gctgaaaatt 1080
cactggatat gaaaatagtt aatcatgaga aatcaactga ttcaatcttc ctattttgtc 1140
agcgaaggga atgagactct gggaagttaa atgactggcc tggcattatg ctatgagttt 1200
gtgcctttgc tgaggacact agaacctggc ttgcctcctc tataagcaga aacaatttct 1260
gccacaacca ctagtctctt taatagtatt gacttggtta agggcattta cacacgtaac 1320
tggatccagt gaatgtctta tgctctgcat ttgccctgg tgatcttaaa attcgtttgc 1380
ctttttaaag ctatattaaa aatgtattgt tgaatcaaaa aaaaaaaggg agtgagaggt 1440
ggggtggggg gggggaggag ggggggcccgt ttaggggggg ccgggttt 1488

```

(2) INFORMATION ON SEQ ID NO. 53:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2262 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
 ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

000260 092000

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

```

ctcgagccga ttcggctcga gctaattttt aagtctcgat tggaaatcag tgagtagggt 60
cataatgtgc atgacagaaa taagctttat agtgggtttac cttcatttag ctttggaagt 120
tttctttgcc ttagtttttg aagtaaatc tagtttgtag ttctcatttg taatgaacac 180
attaacgact agattaaaat attgccttca agattgttct tacttacaag acttgctcct 240
acttctatgc tgaattattga ccctggatag aatactataa ggttttgagt tagctggaaa 300
agtgatcaga ttaataaatg tatattggtg gttgaattta gcaaagaaat agagataatc 360
atgattatac ctttattttt acaggaagag atgatgtaac tagagtatgt gtctacagga 420
gtaataaatg tttccaaaga gtatttttta aaggaacaaa acgagcatga attactctt 480
caatataagc tatgaagtaa tagttggttg tgaattaaag tggcaccagc tagcacctct 540
gtgttttaag ggtctttcaa tgtttctaga ataagccctt attttcaagg gttcataaca 600
ggcataaaat ctcttctcct ggcaaaagct gctatgaaaa gcctcagctt gggaagatag 660
atttttttcc ccccaattac aaaatctaag tattttggcc cttcaatttg gaggagggca 720
aaagttggaa gtaagaagtt ttatttttaag tactttcagt gctcaaaaaa atgcaatcac 780
tgtgttgtat ataatagttc ataggttgat cactcataat aattgactct aaggctttta 840
ttaagaaaac agcagaaaaga ttaaactctg aattaagtct ggggggaaat ggccactgca 900
gatggagttt tagagtagta atgaaattct acctagaatg caaaattggg tatatgaatt 960
acatagcatg ttgttgggat tttttttaat gtgcagaaga tcaaagctac ttggaaggag1020
tgctataaat ttgccagtag ccacagatta agattatatc ttatatatca gcagattagc1080
tttagcttag ggggaggggt ggaaagtttg gggggggggt tgtgaagatt tagggggacc1140
ttgatagaga actttataaa cttctttctc ttaataaaag acttgtctta caccgtgctg1200
ccattaaagg cagctgttct agagtttcag tcacctaatg acaccacaa aacaatatga1260
atatggagat cttcctttac ccctcaactt taatttgccc agttatacct cagtgttgta1320
gcagtactgt gatacctggc acagtgtctt gatcttacga tgccctctgt actgacctga1380
aggagacctt agagtccttt ccttttttga gtttgaatca tagccttgat gtggtctctt1440
gttttatgtc cttgttccta atgtaaaagt gcttaactgc ttcttggttg tattgggtag1500
cattgggata agatttttaac tgggtattct tgaattgctt ttacaataaa ccaattttat1560
aatctttaaa tttatcaact ttttacattt gtgttatttt cagtcagggc ttcttagatc1620
tacttatggt tgatggagca cattgatttg gagtttcaga tcttccaaag cactatttgt1680
tgtaataact tttctaaatg tagtgctttt aaaggaaaaa tgaacacagg gaagtgactt1740
tgctacaaat aatgttgctg tgttaagtat tcatattaaa tacatgcctt ctatatggaa1800
catggcagaa agactgaaaa ataacagtaa ttaattgtgt aattcagaat tcataccaat1860
cagtgttgaa actcaaacat tgcaaaagtg ggtggcaata ttcagtgtct aacacttttc1920
tagcgttggt acatctgaga aatgagtgct caggtggatt ttatcctgc aagcatgttg1980
ttataagaat tgtgggtgtg cctatcataa caattgtttt ctgtatcttg aaaaagtatt2040
ctccacattt taaatgtttt atattagaga attctttaat gcacacttgt caaatatata2100
tatatagtac caatgttacc tttttatttt ttgttttaga tgtaagagca tgctcatatg2160
ttaggtactt acataaattg ttacattatt tttcttatg taataccttt ttgtttgttt2220
atgtggttca aatatattct ttccttaaac tcttaaaaaa aa 2262

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09646569 "092000

(2) INFORMATION ON SEQ ID NO. 54:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1301 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

```

accagcaagc aaccggccga agtctggaag ggcgccggag ccccgcgaa cggcccgacg 60
gagcgcagga ggttccccgc cgccgcgcgc ttggccccga gtctctgcag ccgcagccgg 120
cacggaggga gccagccccg accttgcccc gctgcggccc gcggctcccc gccaaacccc 180
cctcaggaaa gaggttttaa aatcaaagat gggaaaatcg gagaaaattg cccttcccc 240
tggccagctt gttcatggta tacacttgta tgagcaacca aagataaaca gacagaaaag 300
caaatataac ttgccactaa ccaagatcac ctctgcaaaa agaaatgaaa acaacttttg 360
gcaggattct gtttcatctg acagaattca gaagcaggaa aaaaagcctt ttaaaaatac 420
cgagaacatt aaaaattcgc atttgaagaa atcagcattt ctaactgaag tgagccaaaa 480
ggaaaattat gctggggcaa agtttagtga tccaccttct cctagtgttc ttccaaagcc 540
tcctagtcac tggatgggaa gcactgttga aaattccaac caaaacaggg agctgatggc 600
agtacactta aaaacgctcc tcaaagttca aacttagatt tcagatttca gtatgtgtgt 660
aaaacataat ttttcccata tccctggact cttgagaaaa ttggtacaga aatggaaatt 720
tgccctgttg caacatacaa ttgcaaaaaga tgagtttaaa aaattacata caaacagctt 780
gtattatatt ttatattttg taaatactgt ataccatgta ttatgtgtat attgttcata 840
cttgagaggt atattatagt tttgttatga aagtatgtat ttgcccctgc ccacattgca 900
ggtgttttgt atatatataa tggataaatt ttaagtgtgt gctaaggcac atggaagacc 960
gattttatatt gcacaaggta ctgagatttt tttcaagaaa cagctgtcaa atctcaagg 1020
gaagatctaa atgtgaacag tttactaatg cactactgaa gtttaaatct gtggcacaat 1080
caatgtaagc atggggtttg tttctctaaa ttgatttgta atctgaaatt actgaacaac 1140
tcctattccc atttttgcta aactcaattt ctggttttgg tatatatcca ttccagctta 1200
atgcctctaa ttttaatgcc aacaaaattg gttgtaatca aatttttaaa taataataat 1260
ttggccccc ctttttaaaa aaaaaaaaa aaaaaaaaa a
1301

```

000260" 69594960

(i) SEQUENCE CHARACTERISTIC:

- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) ANTI-SENSE: NO

- (A) ORGANISM: HUMAN
(C) ORGAN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

ccacgtagcc	tctgtccgct	gcgtgcagct	tctgtctccc	tgtttttcta	atcaaggggt	60
taggactttg	ctatctctga	gatgtctgct	acttgctgca	aattctgcag	ctgtctgctg	120
ctctaaagag	tacagtgcac	tagagggaag	tgttcccttt	aaaaataaga	acaactgtcc	180
tggctggaga	atctcacaag	cggaccagag	atctttttta	atccctgcta	ctgtcccttc	240
tcacaggcat	tcacagaacc	cttctgattc	gtaagggtta	cgaaactcat	gttcttctcc	300
agtcacctgt	ggtttctggt	ggagcataag	gtttccagta	agcgggaggg	cagatccaac	360
tcagaacctg	gcagataagg	agcctctggc	aaatgggtgc	tcatcagaac	gcgtggattc	420
tctttcatgg	cagaatgctc	ttggactcgg	ttctccagge	ctgattcccc	gactccatcc	480
tttttcaggg	gttattttaa	aatctgcctt	agattctata	gtgaagacaa	gcatttcaag	540
aaagagttac	ctggatcagc	catgctcagc	tgttagcgct	gaataactgt	ctactttatc	600
ttcactgaac	cactcactct	gtgtaaaggc	caacagattt	ttaatgtggt	tttcatatca	660
aaagatcatg	ttgggattaa	cttgcctttt	tccccaaaaa	ataaactctc	aggcaagcat	720
ttctttaaag	ctattaaggg	agtatatact	tgagtactta	ttgaaatgga	cagtaataag	780
caaatgttct	tataatgcta	cctgatttct	atgaaatgtg	tttgacaagc	caaaattcta	840
ggatgtagaa	atctggaaag	ttcatttccct	gggattcact	tctccaggga	ttttttaaag	900
ttaatttggt	aaattaacag	cagttcactt	tattgtgagt	ctttgccaca	tttgactgaa	960
ttgagctgtc	atttgtacat	ttaaagcagc	tgttttgggg	tctgtgagag	tacatgtatt	1020
atatacaagc	acaacagggc	ttgcactaaa	gaattgtcat	tgtataataca	ctacttggtat	1080
gcctaaactc	atatatgtat	tcttaattgc	acaaaaagtc	aataatttgt	caccttgggg	1140
ttttgaatgt	tgtctttaag	tgttggtcat	ttctatgttt	tataaaccaa	aacaaaattt	1200
ccaaaatacaa	tgaaggaaac	caaaataaat	atttctgcac	ttcaaataaa	aaaaaaaaaa	1260
aaaaa						1265

(2) INFORMATION ON SEQ ID NO. 57:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 274 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
attgcgagtt tttttgtttg ttgtttcaat gtgacttgtc gtttatttca atgaaaattt 60
aaatgattct tacaaatcct ctgaaaagta aaactgatac tttataaac agaagtatat 120
gcaaacagtc acaatatgca ttaggacgac tgacgatatt tcttacatgc caggagattc 180
ttccatccca gcaaacacct cttatctgaa agtgtttttt ctctataaaa ttggcatcta 240
agggattttt aaaaagtcaa aaacagtggc aggg                                274
```

(2) INFORMATION ON SEQ ID NO. 58:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2073 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 53554960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

taaatttcca aatgttctact cgaggatctt agaaaccaaac catacagacg agccgatgcg 60
 gtgaggagaa gcgtcaggcg gcgctttgat gatcagaact tgcgttctgt taatggtgcc 120
 gaaataacaa tgtgaacctg agactggcct gcatgaatac aggggtgtgcg tgaatgaaac 180
 tgcccacatg aacttttatgt gctacgattt aactgcagcc ttgaacacac acaaaaatat 240
 tcttaagggc tcagatttag caaacacaga agaatttttaa aatgagctct cttttcaacc 300
 cttgttaaca agtgcctaaa aatggaagta cctgttcaga ttaatcaaag caataggatt 360
 tgatttgatt aggtatcttt ttacaccagt atgttatatt taaccaaaat gtaaagtctt 420
 tattaaactc attacctgcc attgtgattg tcccatcatg gccacctgg tttcctgatg 480
 ttgtaaataa catcaatgca tctgctgtgg gtcccttgct gagatgtctt cgaaggaatt 540

 ttgttttagc catatccatc aactttgtat tttacttgca atttggaga aggaaagtca 600
 catgatgaaa ctccctttgt ctataaccag gccctggcaa agtgcaaca ggatgcaact 660
 gcagtggcac aaaggctcact caatcccttg tttccagttt cacattctac tacttctgtg 720
 ctagagaacg atgctctgtg agaggcattc actagtatga atgtggggat atagtgtata 780
 agacttattt gcagtactgt gttcttcagc tagaggcagc tttttaaata atgcaagtgt 840
 atttatttagc attaaaatta acatctcagt aatcagcatt agcatttctg aggaccatta 900
 ttaattctga gaacagaaat tgggtgccttg caaggaagtt tactagctct atcaacaagc 960
 attcaaggtt acatctgcta gcagagtagt gttaggaacc tggccttact ctccctgtac1020
 aatcgcaatt ttttcttatt ttttataaat tcaagaagat acacttggca tctgttatcg1080
 aggctaagtt tttcatgcat ttcccagact acttatggag aattgcagtt taagttgctg1140
 aaaagtatta acatgggtatt aagcttaaat aatacgtaat gggactagat ggccactaal1200
 gccactgtta ttttccctcc tctctggcag ggcacttgat ccattccaaa gtcaaaaact1260
 ggactgaagc taaatttgta cttttcataa tatacattct gcttctggct tatcttcttg1320
 gtacatcaat atattaattg taaagtttat tgtatagtat ttaaccgctg aagttcctat1380
 tttatgttgt gcttatgtga accccttggt gaaggtcctt tttccttgga tgtgtagtta1440
 tatgatcttt ttaaagtgtac agatattttg ctataaaatc ggtgcagttt tttatggttt1500
 ttacacttct ctttaattcc cacctaagcc tctgggtaat attgtaaata ttgttttaaa1560
 atgcatcagc ctatgtata caatctgaat gttattttta cttatagttt tttttaatat1620
 atatatttaa ctataaggac agtttaggga acaagttacc taccacattt cacttttagt1680
 tacctattta cagaaagatt aaactgccac ctgcgggcac attcccataa atgtgtactt1740
 tactttaaaa agaacatgcc acgattttgt ctttctgtgg actcaacatt cacttcgatt1800
 aaaaatagca atttgaccaa gttggacttc cactacaaag cagctgtttt ccaaagttca1860
 atgctgacat atatgtatat taaaataatt gcctatttat taatctacaa atagacaacg1920
 ttggcatgtt cttttctgtt tgtctattaa tgggcctgct tcttagcaat attagaatgt1980
 tttataaaaag caattcatgt tacttttctg gtcttttcat ggcatatgag caaataataa2040
 actattttaca ctactagaaa gaaaagagaa gaa 2073

(2) INFORMATION ON SEQ ID NO. 59:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 850 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

```

ctattacaca tgagggttttt aatgtattta gacctgacaa taggggtgtc acttagatgt 60
gatctcagtg ttgtgggttaa ctttgtgtgt ctttaattcg aaatctggaa catagatgat 120
gattttttcc tttgaatttaa cttaatgtgt tctcttccct acagatttca gaacttatat 180
ttccacctct tccaatgtgg caccctttgc ccagaaaaaa gccaggaatg tatcgaggga 240
atggccatca gaatcactat cctcctcctg ttccatttgg ttatccaaat cagggaagaa 300
aaaataaacc atatcgccca attccagtga catgggtacc tctcctgga atgcattgtg 360
accggaatca ctggattaat cctcacatgt tagcacctca ctaacttcgt ttttgattgt 420
gttgggtgtca tgttgagaaa aaggtagaat aaaccttact acacattaaa agttaaaagt 480
tcttactaat agtagtgaag ttagatgggc caaacatca aacttatttt tatagaagtt 540
attgagaata atctttctta aaaaatatat gcactttaga tattgatata gtttgagaaa 600
ttttattaaa gttagtcaag tgcctaagtt tttaatattg gacttgagta tttatatatt 660
gtgcatcaac tctgttgat acgagaacac tgtagaagtg gacgatttgt tctagcacct 720
ttgagaattt actttatgga gcgtatgtaa gttatttata tacaaggaaa tctattttat 780
gtcgttgttt aagagaattg tgtgaaatca tgtagttgca aataaaaaat agtttgaggc 840
atgaaaaaaaa 850

```

(2) INFORMATION ON SEQ ID NO. 60:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2091 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

00646569.092000

aagagacaga ctattaactc cacagttaat taaggacgta tgttccatgt ttatttggtta 60
 aagcagtgtg aatagccttc aagcatgtga ataattcttc atcttccccg ccgctttttg 120
 tttctttcag gtagacacct tttaaaatgc agaactaact gaggcatttc agtaactttg 180
 ctttcaaata aataaagtca aatgtatgga aacattttgt gccctactct ccataccccg 240
 tgtactcaaa ttctctactg tatgaattat gctttaagta gaattcagtg ccaaggagaa 300
 cttggtgaaa taaattattt taattttttt tttatctttt acaaagccat ggatttttatt 360
 tgggtgatgt gtgctctgta cacaagccat ttcaatagga tggagctgtt aattattttc 420
 caaagagtaa tagacatgca aaagtttcaa taaaaactgg gccattaaca aataaattaa 480
 taaactaata agcattccct tctagggttt tgccaaactg cctatccaat aacaaatttg 540
 agaatcgttg aaaaagctag ttatattttc gagaaatgat tttcattatt gaaactgttc 600
 tccctagcag gccattttcc ctttttcttg ggagtttagc aagtttagga gagaatagtc 660
 atgaaaagaa aggggaagaa ggggagaagg gaagagggtta aaaaactaagt gctcagacct 720

atgaacgtaa tccctttgct agaaatatct aagagcagct cagcttggtt gaaactgagt 780
 tttgtcatct tccatatttg caggaaggta ttttctgact tgcaatgcag ctagatgtaa 840
 aattttattt tatcatccta gaaagccttg actagaaaaa tgaataaata ttgagggttt 900
 cctgtccata tctggcttgc atgtgccaga aagcagagaa tagaaaatgt aatctccaac 960
 atccaagcat cgaaacccaa ggggtaggca attctatgta ggttttgac atgaagtttg 1020
 gtgcatcttg gtttatgctg gctcaactgc tattaacact ctctggctta tagtctcttc 1080
 attctattag acaagcacgt atcgaacact tgcttcgcac aaggctcttt agttaacaat 1140
 ttagcagcta ctgtttgtgt taaacacact tttcaccaa taggttctga ggcaaacgag 1200
 agcaatgact atttaaagaa aggcctttcc agcatcactt acacatccca aaactaaaaa 1260
 gatcaactct tccaactgag aaaagactcc tggctttgaa tggaaactta cagcagagag 1320
 tcacaggcca cggcaacaac aacgacaaca acaaactttt ggaatattat tctcaactca 1380
 cgttttaata atacatctta ttatttttct agtagagaaa ctacaaatca gcctcttcaa 1440
 catttatata cagtttaata agcctcttgc aagttacttg ttctctcacc tgagggtattt 1500
 ttttctctcc cacttgccc ctgttctctc ctctctcttc tccctttgca agaggaaata 1560
 ttttaacatat ttgggtccaa cttcaataat gtaataatta atacattaaa agcatttaac 1620
 ttcttttcta gaaaaatgca caggctaagg catagacaaa acaaagagaa atgctgagaa 1680
 atttgccact ggagacaagc aatctgaata aatatttgcc aaaagttctt tttatgtcat 1740
 atagtgtcag gatttgaagg agctattttt ttttaatgtt gcaactagca actcatcttc 1800
 ggaagacaca gccaggagaa tgaagtagaa gtgaaagggt tataaatcca tttgtaagca 1860
 tttatcccat atattttaaa ttcaagaaaa attgtgttta tctttagaat tttgtattca 1920
 atactttatg tactatgtga ctcatgcttc tggataaata aagcaccaaa tatgtatctg 1980
 taaccacaat cacacatatt atattaaata tatatctata taacagccaa aaaaaaaaaa 2040
 agaagagaag aaaaagaaag gagagggggg gggagagaag gggggggagg t 2091

(2) INFORMATION ON SEQ ID NO. 61:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2952 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

ctcgccccaa accaggacac cctctctaca gtaaatacat gcgtggggat gtacttgtga 60
 tgctgaagca gacggaaaat aattacttgg agtgccaaaaa gggagaagac actggcagag 120
 ttcacctgtc tcaaatgaag attatcactc cacttgatga acatcctaga agcagaccaa 180

 acgatccaag ccacgctcag aagcctgttg acagtgggtgc tctcatgct gtcgttcttc 240
 atgatttccc agcagagcaa gttgatgatt tgaacctcac ttctggagaa attggtttat 300
 cttctggaga agatagatac agattggtac agagggaact gtagaaacca gattggcata 360
 tttcctgcca actatgtcaa agtgattatt gatatcccag aaggaggaaa tgggaaaaga 420
 gaatgtgttt catctcattg tgttaaaggc tcaagatgtg ttgctcgggt tgaatatatt 480
 ggagagcaga aggatgagtt gaggtttctca gagggagaaa ttattattct taaagagtat 540
 gtgaatgagg aatggggccag aggagaagtt cgaggcagaa ctgggatttt cccctgaac 600
 tttgtgagc ctgttgagga ttatcccacc tctggtgcaa atgttttaag cacaaggta 660
 ccactgaaaa ccaaaaaaga agattctggc tcaaactctc aggttaacag tcttccggca 720
 gaatggtgtg aagctcttca cagttttaca gcagagacca gtgatgactt atcactcaag 780
 aggggagacc ggatccagat tctggaacgt ctggattctg actggtgcag gggcagactg 840
 caggacaggg aggggatctt cccagcagtg tttgtgaggc cctgcccagc tgaggcaaaa 900
 agtatgttgg ccatagtacc gaaggggagc gaaggccaaa gccttatatg atttccgagg 960
 ggagaatgaa gatgaacttt ccttcaaggc tggagatata ataacagagc tggaatctgt 1020
 agatgatgac tggatgagtg gagaacttat gggaaaatct ggaatatctt ccaaaaacta 1080
 catacagttt ctacagatca gctagaggag aagcttgtct gtgttccttg gcacaagaac 1140
 tcacttgaac tatcaccttg actatcagat atgtttttgc actatttttt ttaactgaaa 1200
 aagaaatata taagctgtac atggtacact agaattttct gaaagcagaa aacgttcaga 1260
 ttttgtagtt aattttcatt acaatagaaa catgcacatg gaaacccatg agctaggatt 1320
 ctaccgagga aaacatctag tgggattagc aaggtgaagg gaaagcatct ggtggcatgg 1380
 cagcatgggg aggtctcacac acagaagttg cacgtggaca tctgttttaa tcagcacaag 1440
 tgaattaacc atgcttcttc atttttttac tttagttaaa aaagaggaca ttaatatct 1500
 tacatgctgt aactatcagg acatggttag caatctcaat ttcatttttg atattcaa 1560
 taattcttac agcttgagca tatcagcctt attaccagag caaatccttc cttcagatgg 1620
 gatagtttac tgactagttg gagcatttgt aagcacatgg tgaaatcagc ccctgccac 1680
 caaaaataatc tttatgttac caagtgatcc ccatttgtct aaggatttga agggggtcta 1740
 aattggatgt atcttagtct aaagaaccaa aacctccctt gaaatgcctt gctaatacaa 1800
 ctaatccttc catatatgtg ccatacttat ttttttctc agtgtatact ttatgttaac 1860
 agggttatta caaagcacat tttctgaatc tgcaatcatt cctttgacaa ttactggacc 1920
 caaaggaaaa ttcattttct ttgcattatt ccagtaatat ataaaaactg tgtctgttta 1980
 tagtagtaca ttatgaatca catataaaat cttacaatac agaacaactg ttaagatgga 2040
 aaacagtgcc aaacctccac agctcatttc tttgtaatat aatcagaatg aaaaataatt 2100
 taagaggaca gaagactggg acttttttgt tttatttttt ctctagctta tccctgcaca 2160
 attattagag tgaatgaaaa accactttcc tgctttccat tgttataaat tctaagctta 2220
 agataaaagt ggttctttac atgactgaat caattacaat ttatgggcta gagccaaata 2280
 ggttgaagac aatcatccaa acagatcaat ggaatagaat ttcattggaa atgtaaaaca 2340
 ctttcccaac aatggtcatg actttcttct gtttttgaga agagtttcat atgctggacc 2400
 acattttagc ttttattgtt tttttttcc cattgtccaa aaagttaagc aacaagtggc 2460
 cacactttta cgtgactaca acctggagtt ctgcaaagaa ggtaatat tttactgtct 2520
 tgactaaaag tatctcccca ttctatggtt acattttatt ttggactatg gggacttcta 2580
 atacgttttg gtaaagaaga gagtataaag aaaattcttg tcaaatttca ctcaaaagta 2640
 atttcatgag aaatcaatga tttaaagcat tatccaaatt aaattatcat ttgcagcaaa 2700
 ctgtacaaca gcaggaagga tatggaatgg aacatgaggt atatatcttt gcctttataa 2760
 ttttaacatc ttatattgaa gattctgaaa acctatcttt attagaggaa aatctcaatc 2820
 ttcagttttg gccttctgtc accagaatga taagtgcatt agttgtaaat ctacttgaca 2880
 ctgtaataaa ctgaactgaa ctttcaaaat ccctttctca tactagactg agttttttga 2940
 gaatggaggt gg

2952

(2) INFORMATION ON SEQ ID NO. 62:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2313 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

09646569.092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

cataatagtt aactctactt actgttttta catacatttg atttaacaaa ttgttcagca 60
 taacacttct aattaagttt atcaagttgt actgtattag ataatcagca gtgtatctgg 120
 agtatgttta aagagaacag ttcgcaatac aaaaagttac atggagcttt acatcttaac 180
 tttctttgtc aatttaaagt caatgtataa aaagtttatt ttgctattgt gaaaaactaa 240
 atgtaaagga aatcacctac tttcatgcag gtgtataatc ttgaaaagga aaaatgcttc 300
 catgttgaag ccagattttc tgtagtaaaa cttttaaata ttattttaaa agaaatatgt 360
 atataaatat ctctatatct tttggaatga tactaaagtc tctgggtctag gaccatacct 420
 tatataaagg tataagagac catgacaatg tctgaaaatg gaatagataa tgatgccttt 480
 tatttaaaagt ggcccacata atatacattg agtactccat ctctccaaat gtatttccat 540
 aatgtgttga aaacatgcta acatttgtat gattttttata cttctgccga atagacttag 600
 aatcagatga attgtctgtg tgtcttgcaa aagagttggg gacaacttgg gcaggcctat 660
 gaagtgcata gggagtgtat gtcttctgaa tgggttttatt gttcttgtaa tctagcttaa 720
 agaaatgtta actgggaggg tgctgaggcc actcactgca ttaattttgt gtgttttagag 780
 ttctgttgtc aaaagaaaac taatgaataa attagtttgt cattctagaa tttaaagtcc 840
 taagattagt ataaagagta tatagattgt taatccccac cagctagact ttgaacttaa 900
 gtcagactta aagatttgag aaattatttg tgtcatttac tagacgtgat ttttagttct 960
 gtttgattat atttctaca caaacttctt atttaacagg atagcctact aaattaaatg1020
 tttcttattt cacttaactc atttgattaa actgtattct aaaacatttg ggggttttcc1080
 ccttattcag ttttaatctt ggaatatgca tttgtaaatt gtgatgtcat tgagactatal1140
 tttatatattg acttggaac attaacatgt cctaagactt agtgcagaga agcttggcag1200
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 tgaaagcagg gaaaagaatt tccttttccc ctttttttgt gttgtctata ggaattaact1320
 tgggattgtt ttgtgggttt ttgtttgttt taaatgtaaa ttgagaatct tttataagaal1380
 ataaaagcat tattgggtgc ctttgtttgt aaaccaaaaa gtaataaatg aatccctatal1440
 tttccattat agtattttat gtattttttat gttctgaaaa ttacccatgg aacaatatgc1500
 ttaggattac aggaagcagt ccttacttac acttcttgtc tgttttaggt gtacttgtaa1560
 attcttatgt cctaatttta ttttaattctg agttccttac acagcatttt agggaaagaal1620
 tacaggcagg atgacacttt gtgttaaagt gttattttta tgtattacct ggaatgaggc1680
 aggttttttt ctgttttcta aaaagagtaa ccaagatacc tccagggtgt cattgggttc1740
 cagctgctct cctccacatt gaatgatatc ttgttaattt ataggcacat ttgtggtaat1800
 ttatatgtct atagagtaag tataagagat aattcattag taataggaat taactgacct1860
 cttttggatg ggggagagca tcaggctggg gtcaggtaag tgtaaatggc cttctgagca1920
 tgctcttcta ggctgactcc cagccctgac ttgaaaccat tagcgctaac ttgctctgtt1980
 ttgagaaaaa ctttccaaac ttttgcatga gaaactagaa aaaggaatgt atgccacgta2040
 actggattac agaaatgagt taattgtctc tgtgataaaa aaaaaaatg aaatattttc2100
 ttattgaatt aatatttttg tcttgaagca ttttctagtg atagaatgta tttgtctttt2160
 ttcttggtgg taccctctta gcatatatct ttgctatcct taagatccta aacaaatcat2220

 ctttgtcagt taagtatagt tgcgcaaaaa ttgttaaata ctttgtcttt attaaagaaa2280
 aatttgagta acaaaaaaaaa aaaaaaaaaa aaa
 2313

000260"69594960

(2) INFORMATION ON SEQ ID NO. 63:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1650 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

```

ccgcggggct gggggagctc ggggagcctg cgggaccggg ggagcccga ggcaggggg 60
atcccgcggc ggcgccaggg aggcggagga gcaggcgggt gaggcgaggc aggaagagga 120
gcaggacttg gatggtgaga aggggccatc atcggaaggg cctgaggagg ggggacggag 180
aaggctttct cttcaaatac agccccggga agctgagggg aaaccagtac aagaagatga 240
tgaccaaaga ggagctggag gaggagcaga gaactgaaga ataacgaagt tatccttagc 300
gtcctcctaa aggtttttcc ttttggcatc ttaaaagctt gagagataaa acggaacccc 360
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gccctgtgta gagatgttca tgtctgttcc tgtgggtcac tttgttaagc tgaagagttt 540
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cacacctcat gtactcctca tggcttggat ctctgtattc agcctttgtt cagtccaata 1560
aactttgagt agatgatctc aaaaaaaaaa aaaaaaaaaa gggagaaggg aagaaggaga 1620
gggcacaaag gcggaatggg ggtgagcttt

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1650

000220 " 6954560

(2) INFORMATION ON SEQ ID NO. 64:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2851 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

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cgccccgcgc cgccccgcgc ctgtcagctc cctcagcgtc cggccgaggc gcggtgtatg 60
ctgagccgct gccgcagccg gctgctccac gtcctgggcc ttagcttctt gctgcagacc 120
cgccggccga ttctctctctg ctctccacgt ctcatgaagc cgctgggtcg gtctgtcctc 180
ggcgggcccc gcgcgggcaa ggggacccag tgcgcccgcg tcgtcgagaa atatggctac 240
acacacccctt ctgcaggaga gctgcttcgt gatgaaagga agaaccaga ttacacagtat 300
ggtgaactta ttgaaaagta cattaaagaa ggaaagattg taccagttga gataaccatc 360
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000250" 6594960

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 gtattgctaa gtactataac atattggcca ctaaaattca tattgagatt atcttggttt2280
 cttggaagag ataggaatga gttcttatct agtgttgagc gccagcaaat acagaggtgg2340
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 gttgattgag ataatatgac ttaactagtt ttgtcattcc atttggttaa gatacagtca2700
 ccaagaatgt tttgagtttt ttgaaagacc ccaatttaag ccttgcttat ttttaattaa2760
 tttccattca gtgatgttgg atgtatatca attatttagt aaataatctc aataaatttt2820
 gtgctgtggc ctttgctaaa aaaaaaaaaa t 2851

(2) INFORMATION ON SEQ ID NO. 65:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1071 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00646569.092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

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attccaaaca tggcggctcc actagggggt atgttttctg ggcagccacc cggccccctt 60
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agaccttcca gcagtacttt ggtggacgag ttggagtcac ctttcgaggc ttgctttgca 180

tctctgggtga gtcaggacta tgtcaatggc accgatcagg aagaaattcg aaccgggtgtt 240
gatcagtgtg tccagaagtt tctggatatt gcaagacaga cagaatgttt tttcttacaa 300
aaaagattgc agttatctgt ccagaaacca gagcaagtta tcaaagagga tgtgtcagaa 360
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cattggcagc aggtgctgga ggacatcaac gtgcagcaca aaaagccccg cgacatccct 480
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acgtgagcaa agggcagagg cagttggcct atgagtgggc tgatgcgtga ggttggccac 600
acattccttc ctgtggactt gacatttttg aagaactctt tgccagataa tgagttcatt 660
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gtactttata acatgtctgt agcttgata aaccaagtaa gtattttttt tttgtcttta 780
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tacctcaaga agaggaatct aatacaatat ttgtaatgtt tccagaaaaa a 1071

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(2) INFORMATION ON SEQ ID NO. 66:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2375 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260 "69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

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agcttgccaa ttctgtaact ccttgggata tcttgctgag ctttaattgca gctgccactc 60
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caactttata caagaatacc tcagtactgg aaaatcacca ctggagatct gcagtgggct 180
tattgagaga atcaggctta ttctcacatc tgccattaga aagcaggcaa caaatggaga 240
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tggttttaca gatggctttg aaatgtgctg atatttgtaa cccatgtcgg acgtgggaat 420
taagcaagca gtggagtga aaagtaacgg aggaattctt ccatcaagga gatatagaaa 480
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tccagattgg ttttatgact tacctagtgg agcctttatt tacagaatgg gccaggtttt 600
ccaatacaag gctatccag acaatgcttg gacacgtggg gctgaataaa gccagctgga 660

agggactgca gagagaacag tcgagcagtg aggacactga tgctgcattt gagttgaact 720
cacagttatt acctcaggaa aatcggttat cataaccccc agaaccagtg ggacaaaactg 780
cctcctggag gtttttagaa atgtgaaatg gggctcttgag gtgagagaac ttaactcttg 840
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00646569 "092000

(2) INFORMATION ON SEQ ID NO. 67:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1823 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

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gagtttgcaa gaaacaggtg cttaacacta attcacctcc tgaacaagaa aaatgggctg 360
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caagtcaaaa tcttctatgt tccaagtcag aactttgaga gaactgttat ggggctatag 900
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1823

09646569-092000

(2) INFORMATION ON SEQ ID NO. 68:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2403 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000250" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

tgaaactcct gttttccgaa gatcagcaag gcggttctct ggaacagctg ctgcagaggt 60
 tctcatcaca gtttgtgagc aaaggcgact tgcagacgat gctgcgagac ctgcagctgc 120
 agatcctgcg gaacgtcacc caccacgttt ccgtgaccaa gcagctccca acctcagaag 180
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 tatataaatc aaaatttctt atataaaaact gatttgggat ttgggggtgga aatattttga 2220
 atattaatth attttttaaag atgcaagata ggactttgtg caatgtattt ttgtaaatgc 2280
 ttttcaaaat atctgtcttt ggtagtgtt ctgctgtctg caccaaaattg ataagatgct 2340
 attaagaggt ttaaataaag agttttaatt tttaaaaggg aaaaaaaaaa aaaaaaaaaa 2400
 aaa 2403

(2) INFORMATION ON SEQ ID NO. 69:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1246 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

```

actaagattt tatgttgagg atacttcttt aaataaccta cagcttgggt ctatggcttg 60
tgacccccag attcatggag gggcttttagc aatcagcttt gtacatcatc atttttctga 120
atgaccaatc ccactaaaca tctttgaagt cggcctagag aggtccttca gatgattcag 180
aaatagctgg cttgtctgag tccagatttc tcatcaactg gcaatacaaa ggaaaatatg 240
gtacaggagt tagttagaaa ggtcttattg attttacttc tacttttcac tacagttaca 300
ggtagaatac tgtaggaagt cagtgcgaag tgcattgctt attgatagat attgattggt 360
tttcagttct tggggtcagt tttgtggttt ctgctttctt gcctaaatca aagactatgt 420
caagtcaaca acactgaaaa ctgcttttgc cctccactct tacagctgtg cctaataata 480
attaattaat aaacgcacag ccctatgtga acagacagga atttcttggt caatgtggag 540
caaattggaat ggtctccttc cgcaagtctt ttttaacctc atatctggag tacaagggtg 600
gacctctggc ttaccacata cactatgcta aagtcattcag ccactgctac tacatcttgc 660
cagaagggtt ccctcgccaa caaacagttg aaatttaagg gaagaagcaa aagctaaact 720
gtctttgacc ctaagataga tagaaagcta tttatttggt ttcagtgttc aaggcatgac 780
tagtatttct aattagccta ataaattccc acactttctg aagtgaacac taatggtatt 840
gtcctactaa aactgtcatt gtttcttttt ttttaactgg tcagtcatc acaataagct 900
atgagggtaa ataaatatgt gttataacaa gtaaaccgta gttgcaagaa tataccatga 960
agattaaagt aggctgggtt tcatttccat ctcccccac atctcattga atttgatggt 1020
tgacttaatt ggcaccataa ctttgatga tattatacat taacctttat ttatgtaaag 1080
taaaatgcct tatatattaa agagtaagtg caataatatg aaatagcctg tacattttaall 1140
aaatgttgct accaagttat ataaatccac atctctgtaa acaacctttt ttaagtaatt 1200
ttaaaaaaaaa taaacactct gcttactact tgaaaaaaaa aaaaaa 1246

```

(2) INFORMATION ON SEQ ID NO. 71:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1950 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

000260 69594960

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

```

ggggtcgcgg gccctgattg cgccgtttcc ccgcgcagag ctgcgcggcg ccccgacggg 60
ccccggagca gcggcccccg gccggcccg cctcagcctg gagctccagc taccacatg 120
caccttacct gggttccgcc cggtccctga gtccccacaa aatggctgat ggaggaagcc 180
ccttcctagg tcggaggggac tttgtctacc cttcctcaac ccgagaccct agtgctcta 240
acggaggggg cagcccagcc aggagggaag agaagaagag aaaggccgcc aggtcaagt 300
ttgacttcca ggcgcagtcc cccaaggagc tgactctgca gaagggtgac attgtctaca 360
tccacaagga ggtggacaag aactggctgg agggagagca ccacggccgc ctgggcatct 420
tccctgctaa ttatgtggag gtgctgcccg cagatgagat ccctaagccc atcaagcccc 480
cgacctacca ggtgctggag tatggagagg ctgtggccca gtacaccttc aagggggacc 540
tggaggtgga gctgtccttc cgcaaggagg agcacatctg cctgatccgc aaggtgaacg 600
agaactggta cgaggagcgc atcacgggca cggggcgcca aggcatactt cctgccagct 660
acgtgcaggt gtctcgtgaa ccccggtccc ggctctgtga cgacggcccc cagctcccca 720
cgtctccccg cctgaccgct gccgcccgt cagcccgtga cccagcgcc ccctcagccc 780
tgcgacgccc agctgacccc accgacttgg ggggacagac ctccccccgt cgcactggct 840
tctccttccc caccagagg cctagacccc agaccagaa tcttggcacc cctgggtccag 900
ctctgtccca ctctcgaggt cccagccatc ccctggacct ggggacctcc tctcctaaca 960
cctctcagat aactggacc ccgtaccggg cgatgtacca gtacaggccc cagaacgaag 1020
acgagctgga gctgcgcgag ggggacaggg tggatgtcat gcagcagtgt gacgatggct 1080
ggtttgtggg tgtctcccgg aggacccaga aattcggaac gttccctgga aattacgttg 1140
ccccggtgtg agtgggtctc atggcaactt ggagccagcc aggatggggg ggggagcgg 1200
ggcactcgtg ggaggagag gacccccgcc cacatcctcc ttcccagga cctgagctcc 1260
cagcatctgc agacgacccc cgcagcattt ccctcggacc cccctcgaag cccctggac 1320
tgattccca cccagactca caggcattcc tcccacagcc ctttcatttc ctccccaccc 1380
cactcccaaa atacagaggt ctgctttgaa gcggagacca tttccaggcc ttattgagac 1440
cagaccccaa gtccccacc cccatcctgc tccagcgttt cctctaacag ggaccagctc 1500
tccgctttgc ccccacgggg ttcccttaac cagaaccagc ttccctagct cgtagagacc 1560
aaaggccgcc ccgcctgct ggggttcctc ccagcacccc agcttgctgg ctgccctctt 1620
tgcccttctg cctccagctg ggtgtggggg gcgggacaag gcgggggaca gacgcagcac 1680
cttcttagcg atctaggcct ggcaagagct ctggcccaaa ggctcctct tcccaggggc 1740
tgccaagtcc tggccctggc cctggcatat caccgcgcac tgtggggcca ggcaccacta 1800
gcctggctca aatattcccc agggagactg ctgtgtgctg cccgcctgcc tgctggctct 1860
ccccagccc cacatccct ctggaagaga atgtaaaata aacctggaca caagggaag 1920
aaaaaataag attggggggg aggaaaaaaa

```

00250"5954960

(2) INFORMATION ON SEQ ID NO. 72:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 814 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

```

cgggggagag cggggcctgc gcggtagtgg gacccgaccc tgtctccagt gggcgtcttg 60
ggccccgggt ctattctggg ctgcgggcct gggaagggct cgccgggtgc caaatgagct 120
gtcctaactc tgcggggctg cagcttcctg catgatgctg gggagcttgg cgcctgaccc 180
aggatctaga aggcactctg ggcaggccgc gtcgcgccc cgaaggtacc caaccctctg 240
ggatagatgc aggaagcgat ggtaagacc cattttcacc caacttctcg ccgcagtctg 300
gcttaccaca cgctcctccc cattcccagt gagccgcttt ttgcagcacc aggcgaacac 360
ttacaccagt gctttgtaaa ggaatcttat tgtccacccc gtgtcttggc aaaagaacag 420
tgatcacaca gattcctact tgggctcttt cttttaatct tcggaggctg agtttgccca 480
actcaggttt aaccaccaag gactctgaga gctggcagg ctgagtaacc ctggtaacaa 540
ttctcttcac cttatcaaaa cctgagctaa aaccaatgca tcagctgatg atgacagcag 600
agagtggcag ggctgaggac ccaaagtcac ttcccaggct ggcggagaat aaactgccag 660
ggagaagaat gagaagacag gagacaaact gtttgaaag ctaaactctc cctcttaatg 720
aataaagggt tttgccttgt cttaaaaaat aacaggaaga agcagggaaa aataaataac 780
ttatggtaat ctggaattgt attttgtaat atta 814

```

(2) INFORMATION ON SEQ ID NO. 74:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 747 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

09646569 "092000

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```

tggggcacgcc  eggccccgtac  cccggccccgc  tgtcgcgcccc  gccccgaggcc  ccgcccgtgg  60
agagcgccga  gccgctgggg  cccgcggccg  atctgtgggc  cgacgtggac  ctcaccgagt  120
tcgaccagta  cctcaactgc  agccggactc  ggcccgcacg  ccccgggctc  ccgtaccacg  180
tggcactggc  caaactgggc  ccgcgcgcc  tgtcctgccc  agaggagagc  agcctgatct  240
ccgcgctgtc  ggacgccagc  agcgcggtct  attacagcgc  gtgcatctcc  ggctaggccg  300
ccggcgccgc  ccgggtccct  gcagcgcttc  ctcccgcagc  ccccgcgacc  gatccgaccg  360
cgtcgctgcc  gctctgctct  ctcatagcgc  tgtatgtttg  gttccatgtc  acagccccct  420
aggagccagt  gatgctcggc  cttgcgccc  ttccacctcc  caggccaccc  ttctgggct  480
tctggggcac  ctgccctcgg  ggggccccct  cgagggtgcc  tggagtcccc  acgtgtcccc  540
gggcttttcc  aggaagcccc  agcccaggac  ctggtggcag  agttgccagg  gttacatttt  600
tgaagcacct  gtccttttcc  ttgcagtgt  tttctacaa  ccagattgta  ttaatatatt  660
ttactttgcc  cttttaaaaa  atatacctaa  tacaatatat  ttaattttta  attaaactct  720
taaacttttc  ttccaagaga  aaggagc

```

747

(2) INFORMATION ON SEQ ID NO. 76:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2419 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

000260 " 69545569 " 092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

```

cttttgccac ccagtagcgg atagtggacc tgctgggtgga agccgcgggg cccggccagg 60
gatcgtcgca tggattttct ggtggagcct gtccccaagg aagggttccg ggtacctcag 120
gccgagtggg gcagggcagt tctgctttat tcagccctg catgagcgga tgctaaggcc 180
gggtggtctc ctggcctcgg gctgaggcct cttcccggt gtctgcccct ggctgcgct 240
ggacctgcta agtggcccac agtggcagcg aggtcccggt cccggggctg ggggtggaga 300

ccccgggctg agtgcgtggg ctttctggtg gggggcgatg gaaacaggaa accaagcagt 360
gggatcgtag cgttggtcac tgcgaggcga gtggcgggct ttctgtttct gccttggtccc 420
tccccacggt acctggttcc caggtgaaaa tgaaaggagg ggagaagttg agaacagaac 480
attccataaa ggatatttcc taataggctg caagatgctg atgccgagaa tgatgatttt 540
ctttcctgca gatgaaacta ttagaaaagg tcttagattg tggcaggtag gctttggagc 600
aggcgccgag acatttctga gcatgaggac gagctacagc agctcctggg gtggggctgc 660
ctgcgggatg gcgggagagg atgccctgga gaaccgtcct cccagtgtgg aaggcccttt 720
tccctgagga gtgggcattc tgggccagcc ggcgtgtgct tctgtcctcc acgtgggcca 780
gccccagctg ctccgtgttt cctggcggtg gcaatttact gtgctgctga gtgtgaggtc 840
atctccggag cgttttccagc agcccttgcc tctgcggcgt ctcttccggg ctgtgggcat 900
gcaggggaagt ggctgtgagg cagtctgcgc tgtggccctg cctctgccc cgcagagggc 960
gtgggctctg gacaagccgc ccttcaggct ggggtagcag gtcagtccag gcaggaagca 1020
gcacctgccc cccgcgccag cccagcccca gcctgagtgc aggagctgca ggaccccgcg 1080
gggcttttcc agctactctg ttccttcacg tctccttcc tcagcctcgt ccaagcaccg 1140
ggaagacctc caggctgacc ccttgagcag cagtcagcac aggtgcgtgg gggcgtgagg 1200
gaggcagggt cttaccaca ggcgccttcc tctgtccttc ctgctcttcc ttctctgccc 1260
aggccgctgc agctgcacag cctctgctac acctgggctg cctgggaggc ttctgtgtgt 1320
ggtgtctgga cccacaggcc ttgggtcatc ctgtggctgg tctggggtgg ggtctgttgt 1380
ggtccttcca cgggtgcagt ggctgaagt ccctcgcttt tggggggggg gtctctcacc 1440
cccaggccac atagggccag tggtaggggt tccctctatg tcgggcagtg ctgagggtgt 1500
ggatgctctg tgaccccagc tggagcccac acctaaaggc tggcatccac atcatttcac 1560
cctgcagtga ggggaagagg caccagggtg cagcacagcc acaccggtc ccacgtcaga 1620
ggagggcaag gctgggtact cagcagccac tctgagccgg ggctccttcc aggagctgaa 1680
atccacctgt ctccatcttc cttgcctgcc tgggtactca tgccaagcag agactgggat 1740
taggggttct gtgctcttgc ctaattagga acatttccc atgtctcttg tgtgtccca 1800
gaaggagaag tgagtttgcc aaggatatgg ggcaggaggc tccctctgct gacccctgc 1860
agcctggagc cagcccgggg actgtcctgg gtggagggca ggtgaacaca agctgctgcc 1920
ggggactgtc ctgggtggac ggcaggtgaa cacaagcggc tgccgcatgt agccactcac 1980
tcgacttttt ttcagctgtg accattcctg ggagctcttt gagcctttct gtctcatttg 2040
gaaccagggg gaaccaggaa ggggtcctg gcctctctgt gtccctctga gtgggggttg 2100
tggggggcgc agatccacgc cttgctgccc ttctttcatg aagtctgttt tttaagtgt 2160
ggttcccccg aatattttat gcagaggagg gaaaatttat agtggcaatt attttctcac 2220
agtctggtga gcaggcaatt aattaggagt aagggggcct agtagagcgt ggcgtgtggc 2280
agaatcgcac cgcctcggt cccagccca ccgcatgca gggctcgct gcgggaaaac 2340
taatatgccg gcgtttaagc ctgtgcccct ctgctgggtg taactgcgct gaaataaatg 2400
atctgacaat gtgaaaaaa
2419

```


- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RPRLYKAKRK TTNGVVLCCI ALHKIRNRCL TIEFVFCEF

39

(2) INFORMATION ON SEQ ID NO. 80:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

KTPSLQSKTK NNKWSCAMLY CFAQN

25

(2) INFORMATION ON SEQ ID NO. 81:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 29 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

DPVSTKQNEK QQMELCYVVL LCTKLGTGV

29

000260"69594960

(2) INFORMATION ON SEQ ID NO. 82:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

PKRRVSDTSS GPTPCMEPIL GRTHYSQLRK KS

32

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

LGQDSHQHIT HVLLGREKQY IPVERSQSIG GRNVVKGGRG YAAAPSVPEV AVIP

54

000260"69594960

(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 54 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GDQAHREQGK EQAMFDKKVQ LQRMVDQRSV ISDEKKVALL YLDNEEEEND GHWF

54

(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 116 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GTRHPLSLSH KPAKKIDVAR VTFDLYKLNQ QDFIGCLNVK ATFYDTYSLS YDLHCCGAKR 60
IMKEAFRWAL FSMQATGHVL LGTSCYLQQL LDATEEGQPP KKGASSLIPT CLKILQ 116

(2) INFORMATION ON SEQ ID NO. 87:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 71 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

000260"6954960

(vi) ORIGIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

NRGGVGFGVG WSLPFELLIF MSRLQNSRVG LTMWGGGGSS LFFYFQVHSW GWWGGRRIPL 60
PKPLVCAELA L 71

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

YRHEPLYPAF PYKIQRENFY TFIPQIKQVL SSYRALARSI CKRNLKFSCR IKLDK 55

(i) SEQUENCE CHARACTERISTIC:

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

LATHSPQKSH QCAHCEKTFN RKDHLKNHLQ THDPNKMAFG CEECGKKYNT MLGYKRHLAL 60
 HAASSGDLTC GVCALELGST EVLLDHLKAH AEEKPPSGTK EKKHQCDHCE RCFYTRKDVRI120
 RHLVVHTGCK DFLLCQFCAQR FGRKDHLTRH TKKTHSQELM KESLQTGDLL STFHTISPSF180
 QLKAAALPPF PLGASAQNGL ASSLPAEVHS LTLSPPEQAA QPMQPLPESL ASLHPSVSPG240
 SPPPPPLPNHK YNTTSTSYSP LASLPLKADT KGFCNISLFE DLPLQEPQSP QKLNPGFDLA300
 KGNAGKVNLP KELPADAVNL TIPASLDLSP LLGFWQLPPP ATQNTFGNST LALGPGESLP360
 HRLSCLGQQQ QEPPLAMGTV SLGQLPLPPI PHVFSAGTGS AILPHFHAF R 411

(2) INFORMATION ON SEQ ID NO. 90:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 314 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

KRCQRKQPLR GIGILKQAID KMOMNTNOLT SIHADLCQLC LLAKCFKPAL PYLDVDMMDI 60
 CKENGAYDAK HFLCYYYYGG MIYTGLKNFE RALYFYEQAI TTPAMAVSHI MLESYKKYIL120
 VSLILLGKVQ QLPKYTSQIV GRFIKPLSNA YHELAQVYST NNPSELRLNV NKHSETFTRD180
 NNMGLVKQCL SSLYKKNIQR LTKTFLTSL QDMASRVQLS GPQEAKEYVL HMIEDGEIFA240
 SINQKDGMSV FHDNPEKYNN PAMLHNIDQE MLKCIELDER LKAMDQEITV NPQFVQKSMG300
 SQEDDSGNKP SSYS 314

(2) INFORMATION ON SEQ ID NO. 91:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 58 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

VLQEKIKIKK EKKEKIKFKN CFENVQIKSN ILIIHLHVLL NILIMWMFTL CMILA EYH 58

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 201 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

MDLSLLWVLL PLVTMAWGQY GDYGYPPYQQY HDYSDDGWVN LNRQGFSYQC PQGQVIVAVR 60
 SIFSKKEGSD RQWNYACMPT PQSLGEPTEC WVEEINRAGM EWYQTCSNNG LVAGFQSRFY120
 ESVDREWFQF YCCRYSKRCP YSCWLTTEYP GHYGEEMDMI SYNDDYYIRG ATTTFSAYER180
 DRQWKFIMCR MTEYDCEFAN V 201

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 247 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

MGNGLSEERG NNFNHISPIP PVPHPRSVIQ QAEEKLHTPQ KRLMTPWEES NVMQDKDAPS 60
 PKPRLSPRET IFGKSEHQNS SPTCQEDEED VRYNIVHSLP PDINDTEPVT MIFMGYQQAE120
 DSEEDKKFLT GYDGIIHAEL VVIDDEEEED EGAEAKPSYH PIAPHSQVYQ PAKPTPLPRK180
 RSEASPHENT NHKSPHKNSI SLKEQEEESLG SPVHHS PFDA QTTGDGTEDP SLTALRMRMA240
 KLGKKVI 247

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(2) INFORMATION ON SEQ ID NO. 95:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 188 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

MPVLREYLMS GGICPVSRTD IDYLLSKNGS GNAIIIVVGG AAESLSSMPG KNAVTLNRNK 60
 GFVKLALRHG ADLVPIYSFG ENEVYKQVIF EEGSWGRWVQ KKFQKYIGFA PCIFHGRGLF120
 SSDTWGLVPY SKPITTVVGE PITIPKLEHP TQDIDLYHT MYMEALVKLF DKHKTKFGLP180
 ETEVLEVN 188

(2) INFORMATION ON SEQ ID NO. 96:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 290 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

RGAGTQPGPL LKKPYQPRIK ISKTSVDGDP HFVVDFFLSR LTVCFNIDGQ PGDILRLVSD 60
 HRDSGVTVNG ELIGAPAPPN GHKKQRTYLR TITILINKPE RSYLEITPSR VILDGGDRLV120
 LPCNQSVVVG SWGLEVSUSA NANVTVTIQG SIAFVILIHL YKKPAPFQRH HLGFIYANSE180
 GLSSNCHGLL GQFLNQDARL TEDPAGPSQN LTHPLLLQVG EGPEAVLTVK GHQVPVWVKQ240
 RKIYNGEEQI DCWFARNNA KLDGEYKDY LASHPFDTGM TLGQGMSREL 290

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(2) INFORMATION ON SEQ ID NO. 97:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

NQFTSCILFC DGGHWRELLF QSIMSSHWTL KILLVPLFYI SLEFPSGFVL CLANDLGYHF 60
SSRVRS 66

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 54 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

VP GALPLAVG PPPPPSGFPR NVQPRRPSQS LGRVMSAGPD KRPLGTLCCF VSFL 54

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

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(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

FFLYFNQVFY WSGNCKIYKF LKGISCLKAS IALYPRSLIQ TNTQNTKES

59

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 98 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

MGNKEPGSHG HRSDADPSRF SPVLPPAVQL GVVREEGRGG SCFWSWGRGP VSSTWLFPKG 60
SKREGLGEKT MERGPAKENR EEVSGLISLL SRCSGSLI 98

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 117 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

MGKGLGEDGQ QRARESWTSQ RRRPQQVQSR AATSCPAGCL EGRGQRRVMS LQLGEGPSEL 60
HVAFSQREQE GRIGRENNGE GTCEGKQGGG ERFDQPAITV FWLSYLARRL RDRYITS 117

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(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 145 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

MNRGPPPTFWT FEDRGAKRDR SARGPHPAPL GEPLLTWVSL RLHQLVGLQA SPDPSPHCWA 60
 TLNLKFHCPA PPTPTPKFPK EMSKTHAHTY IHTCTCAHTS CVTTGQGNAS LRIPGPGPGV120
 KGCSGTLPPN LLEDPECGGR IGCLP 145

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 197 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

MRTHVLCYHW PRKRESQDSR AWTWGKGLLW DSAPQPLGGP RVWQGDWVSA LTHRISPGPK 60
AEKKSGRRSR RQGWWTKVGV RLKSGSETRF DHTHHPSVPP GQHAPLEPLH RLIRTRQNLL120
LTNLLRAVYR GITLVQEGCP SCFHTTTGPT IPLLASLRP RDPQKPGEKE SWPLVSTAFR180
ATGGDAQMTW VKGLSQT 197

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 152 amino acids
(B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

SEARNAPSGT AQTfamGfMT GTISSMYQTK AVIIAMIITA VVSISVTIFC FQTKVDFTSC 60
 TGLFCVLGIV LLVTGIVTSI VLYFQYVYWL HMLYAALGAI CFTLFLAYDT QLVLGNRKHT120
 ISPEDYITGA LQIYTDIIYI FTFVLQLMGD RN 152

(2) INFORMATION ON SEQ ID NO. 105:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

HLLSPPHILG TAFSSTGNGT DGQKTSITFM KGLLELPGKK ACLGELGRCR QCGWAGGQPV 60
 VLLPAQ 66

(2) INFORMATION ON SEQ ID NO. 106:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

PTSLIWPTTM FCSVHVLFKS ILNWLPSFKL NQTLKAWSSH TGPTFPHGNY ERAPAQQGLS 60
 RSLPPPLPVP QIWPLLRKIR TATGPSEPKP T 91

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 41 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

LLPSFFLHFS LSIYFPHPHF LEQPLVLQEM ALMDRRLALP S

41

(2) INFORMATION ON SEQ ID NO. 108:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 471 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

000260" 6954960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

NELKASGGEI	KIHKMEQKEN	VPPGPEVCIT	HQEGEKISAN	ENSLAVRSTP	AEDDSRDSQV	60
KSEVQQPVHP	KPLSPDSRAS	SLSESSPPKA	MKKFQAPARE	TCVECQKTVY	PMERLLANQQ	120
VFHISCFRCS	YCNNKLSLGT	YASLHGRIYC	KPHFNQLFKS	KGNYDEGFGH	RPHKDLWASK	180
NENEEILERP	AQLANARETP	HSPGVEDAPI	AKGGVLAASM	EAKASSQOEK	EDKPAETKKL	240
RIAWPPPTL	GSSGSALEEG	IKMSKPKWPP	EDEISKPEVP	EDVDLDLKKL	RRSSSLKERS	300
RPFVTVAASF	STSVKSPKTV	SPPIRKQWSM	SEQSEESVGG	RVAERKQVEN	AKASKKNGNV	360
GKTTWQNKES	KGETGKRSKE	GHSLEMENEN	LVENGADSDE	DDNSFLKQQS	PQEPKSLNWS	420
SFVDNTFAEE	FTTQNKQSQD	VELWEGEVVK	ELSVEEQIKR	NRYYDEDEDE	E	471

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 94 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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RKMLRAALPA LPIPRCKYTL FLIAHMGPPY LLALVLMLKS WPOWERCLPGR HSCLVQAKPL 60
CNASPFWCYE VPLCRRFHQQ LVTVPSTRTC FEIS                               94

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(2) INFORMATION ON SEQ ID NO. 113:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 324 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(2) INFORMATION ON SEQ ID NO. 116:

- PDCESFMYFN LDSVFLRVLS MKLADSRQDS FFHHGWLISP

(2) INFORMATION ON SEQ ID NO. 117:

- TNEHTLTSYL QLPFSFNRIV KASCILI

(2) INFORMATION ON SEQ ID NO. 119:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 135 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

RSNAVQLTRM EYAMKSLSL YPKSLSRHVS VRTSVVTQQL LSEPSPKAPR ARPCRVSTAD 60
 RSVRKGIMAY SLEDLLKVR DTLMLADKPF FLVLEEDGTT VETEEYFQAL AGDTVFMVLQ120
 KGQKWQPPSE QGTRH 135

(2) INFORMATION ON SEQ ID NO. 122:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 193 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

EACHTLSCP ALARLGRARR RPWMSHRTSS TFRAERSFHS SSSSSAATS SSASRALPAQ 60
 DPPMEKALSM FSDDFGSFMR PHSEPLAFPA RPPGAGNIKT LGDAYEFAVD VRDFSPEDII120
 VTTSNNHIEV RAEKLAADGT VMNTFAHKCQ LPEDVDPTSV TSALREDGSL TIRARRHPHT180
 EHVQTFERTE IKI 193

(2) INFORMATION ON SEQ ID NO. 124:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 38 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

MATFYPLFPN GGGTYPEVVN DFPLKLLYFT NLNYFVLM

38

(2) INFORMATION ON SEQ ID NO. 125:

(i) SEQUENCE CHARACTERISTIC:

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- (A) LENGTH: 65 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

MWLFHDAGIR SAGGLSLLSC GSWPLPSGYH RLQDTNGQQK NVTLLILSSS SIGTKLPSRP 60
REILC 65

(2) INFORMATION ON SEQ ID NO. 126:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 250 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

ETRVKTSLEL LRTQLEPTGT VGNTIMTSQP VPNETIIVLP SNVINFSQAE KPEPTNQGQD 60
SLKKHLHAEI KVIQTQILC GMMVLSLGII LASASFSPNF TQVTSTLLNS AYPFIGPFFF120
IISGSLSIAT EKRLTKLLVH SSLVGSILSA LSALVGFIIL SVKQATLNPA SLQCELDKNN180
IPTRSYVSYF YHDSLYTTDC YTAKASLAGT LSLMLICTLL EFCLAVLTAV LRWKQAYSDF240
PGVSVLAGFT 250

(2) INFORMATION ON SEQ ID NO. 128:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 61 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

MHTCQIYIYS TNVTFLEFFVL DVRACSYVRY LHKLLHYFFL CNTFLFVYVV QIYSFLKLLK 60
K 61

(2) INFORMATION ON SEQ ID NO. 129:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 211 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

PASNRPKSGR APEPREPARR SAGGSPPPPP WPRVPAAAAG TEGASPD LAP LRPAAPGQTP 60
LRKEVLKSKM GKSEKIALPH GQLVHGIHLY EQPKINRQKS KYNLPLTKIT SAKRNENNFW120
QDSVSSDRIQ KQEKKPFKNT ENIKNSHLKK SAFLTEVSQK ENYAGAKFSD PPSPSVLPKP180
PSHWMGSTVE NSNQNRELMA VHLKTLLKVQ T 211

(2) INFORMATION ON SEQ ID NO. 131:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

MILTNP LKSK TDTFINRSIC KQSQYALGRL TIFLTCQGV L PSQQTPLI

(2) INFORMATION ON SEQ ID NO. 132:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

LGIFLHQYVI FNQNVKFLN SLPAIVIVPS WPTWFPDVVN NINASAVGPL LRCLRRNFVL 60
AISINFVFYL QFGRRKVT 78

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 72 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

MDMAKTKFLR RHLSKGPTAD ALMLFTTSGN QVGHDGTITM AGNEFNKNFT FWLKITYWCK 60
KIPNQIKSYC FD 72

(2) INFORMATION ON SEQ ID NO. 135:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 87 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

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(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

LN VFSS LQIS ELIFPPLPMW HPLPRKKPGM YRGNGHQNH Y PPPVPFGYPN QGRKNKPYP 60
IPVTWVPPPG MHC DRNHWIN PHMLAPH 87

(2) INFORMATION ON SEQ ID NO. 137:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

MYGNILCPTL HTPCTQILYC MNYALSRIQC QGELGEINYF NFFFILYKAM DFIWLMCALY 60
TSHFNRMELL IIFQRVIDMQ KFQ 83

(2) INFORMATION ON SEQ ID NO. 138:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 366 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

RPKPGHPLYS KYMRGDVLVM LKQTENNYLE CQKGEDTGRV HLSQMKIITP LDEHLRSRPN 60
 DPSHAQKPVD SGAPHAVVLH DFPAEQVDDL NLTSGEIVYL LEKIDTDWYR GNCRNQIGIF120
 PANYVKVIID IPEGNGKRE CVSSHCVKGS RCVARFEYIG EQKDELSFSE GEIILKEYV180
 NEEWARGEVR GRTGIFPLNF VEPVEDYPTS GANVLSTKVP LKTKKEDSGS NSQVNSLP AE240
 WCEALHSFTA ETSDDL SFKR GDRIQILERL DSDWCRGRLQ DREGIFPAVF VRPCPAEAKS300
 MLAIVPKGRK AKALYDFRGE NEDELSFKAG DIITELESVD DDWMSGELMG KSGIFPKNYI360
 QFLQIS 366

(2) INFORMATION ON SEQ ID NO. 139:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 68 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

MNPYISIIVF IVFLCSENYP WNNMLRITGS SPYLHFLSVL GVLVNSYVLI LFNSEFLTQH 60
 FRERIQAG 68

(2) INFORMATION ON SEQ ID NO. 140:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 28 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

FFFFFFLLLK FFFNKDKGFN NFCATILN

28

(2) INFORMATION ON SEQ ID NO. 141:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 22 amino acids
 (B) TYPE: Protein

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(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

EGTTRKKDKY ILSLENASRQ KY

22

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 46 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

MPFLRKFDRL VRTSDHQISL KWVSWNFIFD NIYTIPNSFA VLRFVG

46

000260"69594960

(2) INFORMATION ON SEQ ID NO. 143:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

MEGWGMSSIN PYGMHSQWPS HLGLEPLVQG LGENRPHGNS HTVIAFNTEP RVPKQQ 56

(2) INFORMATION ON SEQ ID NO. 144:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

MNISTQGRAK GVPRILLAKG QVLIEGLELS RFMEAACLTG ACPDSSLGFP FYLSSF 56

(2) INFORMATION ON SEQ ID NO. 145:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

000250"69554960

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

MPKGKAFRRT LRITSLFFSS LLLQLLFGH HLLVLVSPQL PGAVFEGEAF SVPPPQALPM 60
 MAPSHHPSFA PLPASPPPPA PPPPWRRRGI PLAFGLPRSR RLPQLPQPR 109

(2) INFORMATION ON SEQ ID NO. 146:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 247 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

RPAPAPRCQL PQRPAEARCM LSRCSRLLH VLGLSFLLQT RRPILLCSPR LMKPLVVFVL 60
 GGPGAGKGTQ CARIVEKYG Y THLSAGELLR DERKNPDSQY GELIEKYIKE GKIVPVEITI120
 SLLKREMDQT MAANAQKNKF LIDGFPRNQD NLQGWNKTMG GKADVSEFVLF FDCNNEICIE180
 RCLERKSSG RSDDNRESLE KRIQTYLQST KPIIDL YEEM GKVKKIDASK SVDEVFDEVV240
 QIFDKEG 247

(2) INFORMATION ON SEQ ID NO. 147:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 181 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

000260"69594960

IPNMAAPLGG MFSGQPPGPP QAPPGLPGQA SLQAAPGAP RPSSSTLVDE LESSFEACFA 60
 SLVSQDYVNG TDQEEIRTGV DQCIQKFLDI ARQTECFFLQ KRLQLSVQKP EQVIKEDVSE120
 LRNELQRKDA LVQKHLTKLR HWQQVLEDIN VQHKKPADIP QGSLAYLEQA SANIPAPLKP180
 T 181

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 236 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

MLRDLQLQIL RNVTHHVSVT KQLPTSEAVV SAVSEAGASG ITEAQAIAIV NSALKLYSQD 60
 KTGMVDFALE SGGGSILSTR CSETYETKTA LMSLFGIPLW YFSQSPRVVI QPDIYPGNCW120
 AFKGSQGYLV VRLSMMIHPA AFTLEHIPKT LSPTGNISSA PKDFAVYGLE NEYQEEGQLL180
 GQFTYDQDGE SLQMFQALKR PDDTAFQIVE LRIFSNWGHF EYTCLYRFRV HGEPAVK 236

(2) INFORMATION ON SEQ ID NO. 149:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 57 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

MEWSPSASLF NPHIWSTRVD LWLTTYTMLK SSATATTSCQ KVS LANKQLK FKGRSKS 57

(2) INFORMATION ON SEQ ID NO. 150:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 52 amino acids
 (B) TYPE: Protein

000250"6954960

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

MHLALTSYSI LPVTVVKSRS KINKTFLTNS CTIFS FVLPV DEKSGLRQAS YF

52

(2) INFORMATION ON SEQ ID NO. 151:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 377 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

LRRFPAQSSP APRRAPEQRP PAGPASAWSS SYPHAPYLGS ARSLSPHKMA DGGSPFLGRR 60
DFVYPSSTRD PSASNGGGSP ARREEKKRKA ARLKFDFQAA SPKELTLQKG DIVYIHKEVD120
KNWLEGEHHG RLGIFPANYV EVLPADEIPK PIKPPTYQVL EYGEAVAQYT FKGDLEVELS180
FRKGEHICLI RKNVENWYEG RITGTGRQGI FPASYVQVSR EPRLRLCDDG POLPTSPRLT240
AAARSARDPS APSALRSPAD PTDLGGQTSP RRTGFSFPTQ EPRPQTQNLG TPGPALSHSR300
GPSHPLDLGT SSPNTSQIHW TPYRAMYQYR PQNEDELELR EGDRVDVMQQ CDDGWFGVGS360
RRTQKFGTFP GNYVAPV

377

(2) INFORMATION ON SEQ ID NO. 152:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 39 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

000260 69594960

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

WDPTLSPVGV LGPGSILGCG PGKGSPGAK

39

(2) INFORMATION ON SEQ ID NO. 153:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 58 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

MQEAMVKTHF HPTSRRSLAY HTLLPIPSEP LFAAPGEHLH QCFVKESYCP PRVLAKEQ 58

(2) INFORMATION ON SEQ ID NO. 154:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 41 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

GGEPGLRGSG TRPCLQWASW APALFWAAGL GRARRVPNEL S

41

000260"6954960

(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

MMLGSLAPDP GSRRHSGQAA LRPRRYPTLW DRCRKRWLRP IFTQLLAHV LTTRSSFPV 60
 SRFLQHQAANT YTSAL 75

(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

GASRACAVVG PDPVSSGRLG PRLYSGLRAW EGLAGCQMSC PNSAGLQLPA

50

000260"69594960

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 97 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GTPGPYPGGL SPPPEAPPLE SAEPLGPAAD LWADVDLTFE DQYLNCSTRR PDAPGLPYHV 60
 ALAKLGPRAM SCPESSLIS ALSDASSAVY YSACISG 97

(2) INFORMATION ON SEQ ID NO. 158:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 173 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

GLFPAVCPWP ALDLLSGPQW QRGPGPGAGV GDPGLSAVAF WWGAMETGNQ AVGSQRWSLR 60
GEWRAFCFCL VPPHGTWFPG ENERRGEVEN RTFHKGYFLI GCKMLMPRMM IFFPADETIR120
KGLRLWQVGF GAGAETFLSM RTSYSSSWG AACMGAGEDA LENRPPSVEG PFP 173

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 109 amino acids
(B) TYPE: Protein

(iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69994960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

GCGGGTGACG CGACGACGGC TCGACACTTT GCTACGGAGT GCATCGGACG TCGAAGCCTA 60
 GAGTCTCTGC GTCTTTCCCT CTTCCGCTGC CTCATTCTT TCCTTCCTAG CCTTGGTCGT 120
 CGCCGCCACC ATGAACAAGA AGAAGAAACC GTTCCTAGGG ATGCCCCGCGC CCCTCGGCTA 180
 CGTGCCGGGG CTGGGCCGGG GCGCCACTGG CTTCACCACG CGGTCAGACA TTGGGCCCCG 240
 CCGTGATGCA AATGACCCTG TGGATGATCG CCATGCACCC CCAGGCAAGA GAACCGTTGG 300
 GGACCAGATG AAGAAAAATC AGGCTGCTGA CGATGACGAC GAGGATCTAA ATGACACCAA 360
 TTACGATGAG TTTAATGGCT ATGCTGGGAG CCTCTTCTCA AGTGGACCCT ACGAGAAAGA 420
 TGATGAGGAA GCAGATGCTA TCTATGCAGC CCTGGATAAA AGGATGGATG AAAGAAGAAA 480
 AGAAAGACGG GAGCAAAGGG AGAAAGAAGA AATAGAGAAA TATCGTATGG AACGCCCCAA 540
 AATCCAACAG CAGTTCTCAG ACCTCAAGAG GAAGTTGGCA GAAGTCACAG AAGAAGAGTG 600
 GCTGAGCATC CCCGAGGTTG GCGATGCCAG AAATAAACGT CAGCGGAACC CACGCTATGA 660
 GAAGCTGACC CCTGTTCTTG ACAGTTTCTT TGCCAAACAT TTACAGACCG GAGAGAACCA 720
 TACCTCAGTG GATCCCCGAC AAACCTCAAT TGGAGGTCTT AACACACCCT ATCCAGGTGG 780
 ACTAAACACT CCATACCCAG GTGGAATGAC GCCAGGACTG ATGACACCTG GCACAGTGAG 840
 CTGGACATGA GGAAGATTGG CCAAGCGAGG AACACTCTGA TGGACATGAG GCTGAGCCAG 900
 GTGTCTGACT CCGTGAGTGG ACAGACCGTC GTTGACCCCA AAGGCTACCT GACGGATTTA 960
 AATTCCATGA TCCCGACACA CGGAGGAGAC ATCAATGATA TCAAGAAGGC GCGACTGCTC 1020
 CTCAAGTCTG TTCGGGAGAC GAACCCTCAT CACCCGCCAG CCTGGATTGC ATCAGCCCCG 1080
 CTGGAAGAAG TCACTGGGAA GCTACAAGTA GCTCGGAACC TTATCATGAA GGGGACGGAG 1140
 ATGTGCCCCA AGAGTGAAGA TGTCTGGCTG GAAGCAGCCA GGTTCAGGCC TGGGGACACA 1200
 GCCAAGGGCG TGGTAGCCCA AGCTGTCCGT CATCTCCAC AGTCTGTCAG GATTTACATC 1260
 AGAGCCGCAG AGCTGGAAC GGACATTCTG GCAAAGAAGC GGGTTCTTCG GAAAGCCCTC 1320
 GAGCATGTTT CAAACTCGGT TCGCTTGTGG AAAGCAGCCG TTGAGCTGGA AGAACCTGAA 1380
 GATGCTAGAA TCATGCTGAG CCGAGCTGTG GAGTGCTGCC CCACCAGCGT GGAGCTCTGG 1440
 CTTGCTCTGG CAAGGCTGGA GACCTATGAA AATGCCCGCA AGGTCTTGAA CAAGGCGCGG 1500
 GAGAACATTC CTACAGACCG ACATATCTGG ATCACGGCTG CTAAGCTGGA GGAAGCCAAT 1560
 GGGAACACGC AGATGGTGGG GAAGATCATC GACCGAGCCA TCACCTCGCT GCGGGCCAAC 1620
 GGTGTGGAGA TCAACCGTGA GCAGTGATC CAGGATGCCG AGGAATGTGA CAGGGCTGGG 1680
 AGTGTGGCCA CCTGCCAGGC CGTCATGCGT GCCGTGATTG GGATTGGGAT TGAGGAGGAA 1740
 GATCGGAAGC ATACCTGGAT GGAGATGCT GACAGTTGTG TAGCCACAA TGCCCTGGAG 1800
 TGTGACGAG CCATCTACGC CTAGGCCCTG CAGGTGTTCC CCAGCAAGAA GAGTGTGTGG 1860
 CTGCGCGCCG CGTACTTCGA GAAGAACCAT GGCCTCGGG AGTCCCTGGA AGCACTCCTG 1920
 CAGAGGGCTG TGGCCCACTG CCCCAAAGCA GAGGTGCTGT GGCTCATGGG CGCCAAGTCC 1980
 AAGTGGCTGG CAGGGGATGT GCCTGCAGCA AGGAGCATCC TGGCCCTGGC CTTCCAGGCC 2040
 AACCCCAACA GTGAGGAGAT CTGGCTGGCA GCCGTGAAGC TGGAGTCCGA GAATGATGAG 2100
 TACGAGCGGG CCCGGAGGCT GCTGGCCAAG GCGCGGACAG TGCCCCCACC GCCCGGGTGT 2160
 TCATGAAGTC TGTGAAGCTG GAGTGGGTGC AAGACAACAT CAGGGCAGCC CAAGATCTGT 2220
 GCGAGGAGGC CCTGCGGCAC TATGAGGACT TCCCCAAGCT GTGGATGATG AAGGGGCAGA 2280
 TCGAGGAGCA GAAGGAGATG ATGGAGAAGG CGCGGGAAGC CTATAACCAG GGGTTGAAGA 2340
 AGTGTCCCCA CTCCACACCC CTGTGGCTTT TGCTCTCTCG GCTGGAGGAG AAGATTGGGC 2400
 AGCTTACTCG AGCACGGGCC ATTTTGGAAG AGTCTCGTCT GAAGAACCCA AAGAACCCTG 2460
 GGCTGTGGTT GGAGTCCGTG CGGCTGGAGT ACCGTGCGGG GCTGAAGAAC ATCGCAAATA 2520
 CACTCATGGC CAAGGCGCTG CAGGAGTGCC CCAACTCCGG TATCCTGTGG TCTGAGGCCA 2580
 TCTTCCTCGA GGCAAGGCCC CAGAGGAGGA CCAAGAGCGT GGATGCCCTG AAGAAGTGTG 2640
 AGCATGACCC CCATGTGCTC CTGGCCGTGG CCAAGCTGTT TTGGAGTCAG CGGAAGATCA 2700
 CCAAGGCCAG GGAGTGTTTC CACCGCACTG TGAAGATTGA CTCGGACCTG GGGGATGCCT 2760
 GGGCCTTCTT CTACAAGTTT GAGCTGCAGC ATGGCACTGA GGAGCAGCAG GAGGAGGTGA 2820
 GGAAGCGCTG TGAGAGTGCA GAGCCTCGGC ATGGGGAGCT GTGGTGCGCC GTGTCCAAGG 2880
 ACATCGCCAA CTGGCAGAAG AAGATCGGGG ACATCCTTAG GCTGGTGGCC GGCCGCATCA 2940
 AGAACACCTT CTGATTGAGC GGTTCCTATG GCCGCTCTCC GTGGGGCAGG GTTGGGCCGC 3000
 ATGTGGAAGG GCTCTGAGCT GTGTCTCTCT TCATTAAAG TTTTATGTG TCGTGTGAGA 3060
 AAAAAAAGA AAAGAAAAA GGGGGCGCCC GGGGGC 3096

0964559-092000

(2) INFORMATION ON SEQ ID NO. 162:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

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CTTTGAATTT TAGAATGTCA TGTGTTCTTT TAAAAAATT AGCTCCCCAT CCTCCCTCCT 60
CACGCGCTCC CTCCCTCCTT CTCTCTCTCT CTCTCTCTCC CTCTCTCACA GACACACACA 120
CACACACACA CACACGCACA CGCACGTCCA CACTCACATT AAATAAAGC TTTATTTGAA 180
GCAAAGCTAG CCAAAATTCT ACGTTACTTT TCCCTTGACT GGATCCCAAG TAGCTTGGAA 240
GTTTTTGTGC CCAGGAGAGT AAATAACTGT GAACAAGAGG CTCTGCCCTT AGGTCTTTGT 300
GGCTGTTTAA GTCACCAACA ATAGAGTCAG GGTAAGAAT AAAAACAATT TCATAGCCTC 360
ATTCATTCAC TTAGAAGTGG TAATAATTTT TCCCTAATGA TACCACTTTT CTTTTCCCCC 420
TGTACCTATG GGACTTCCAG AAAGAAGTTA AATTGAGTAA AATCATCAGA AACTGAATCC 480
ATGTAAGAAA AAATAATTGT TGAAGAAAGA AGTTGATAGA ATTCAAAAAG GCCATCTTTT 540
TGCTTTCACA TCAATAAAAT TTACCAAGTA ATAGATCAGT ACTCACTAAT ATTTTGTAGA 600
CCATAGTTGT CTGGTCAGAA AAATTATATT AAATTAGTAA ATTCTAGAAG CTCTTTAAAA 660
GGGAAGTTTT CTTTCTTCTC CAATTATAGG AGTTGATTTT TACTTTGCAA AGTGGCTCGG 720
TCCTCATGAG CATCTGCATG TTGACTCTTC AGTTAAGAAA ATTGTTGTTC ATTTAGGGAG 780
GTGGATATTC TGATGAAGAT CTTTATCCTA AACCTTCCTA CTATCCTTGT CTTATTCATC 840
AAGCAGATAT TTTAGTCAAG AATTCAGAG AAGGCTGCTC CTAAAATGTC TACTTGACAGC 900
CCAATACCAG TCAATAAAGT ATCCATTCTG GGGTCTGGCT TTAGAAATCA TCTTTGTGGG 960
AAGACCTAAT TCTTCACAGC AAGGATCTCA GGCATGCCTT CTAGATTTGT TCCCTCTGAG 1020
GGGCAGGAAT GAACTGTAGA AATGTTTTAA GGACCCAGAA ACCCCATATG TCTCATTCCA 1080
TGAATATAGG TGAGAGAATT CTTTCCTAAG AGGGTTTGAT ACCAATAGGG GAAAATGTAA 1140
AATGTTTCACT CTTTATGACA ACCTGGCATA AAGGAGTCAA TTCTTATGAA AGAGACACAA 1200
GGGCCTTATG GCCAGGGTTT CTTGGGACAA GACTCTCACC AGCACATCAC ACACGTTCTC 1260
CTTGGAAGAG AGAAGCAGTA CATCCCGGTT GAGAGGTCAC AAAGCATTAG TGGGAAGAAAT 1320
GTGGTAAAGG GGGGAAGGTG TTATGCGGCT GTCCTCCCTG TCCCAGAGGT GGCAGTGATT 1380
CCATAATGTG GAGACTAGTA ACTAGATCCT AAGGCAAAGA GGTGTTTCTC CTTCTGGATG 1440
ATTATCCCA AAGCCTTCCC ACCCAGTGT TCTCTGAAAG CTTAGCCTTA AGAGAACACG 1500
CAGAGAGTTT CCCTAGATAT ACTCCTGCCT CCAGGTGCTG GGACACACCT TTGCAAAATG 1560
CTGTGGGAAG CAGGAGCTGG GGAGCTGTGT TAAGTCAAAG TAGAAACCCT CCAGTGTTTG 1620

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GTGTTGTGTA GAGAATAGGA CATAGGGTAA AGAGGCCAAG CTGCCTGTAG TTAGTAGAGA 1680
AGAATGGATG TGGTTCTTCT TGTGTATTTA TTTGTATCAT AAACACTTGG AACAACAAAG 1740
ACCATAAGCA TCATTTAGCA GTTGTAGCCA TTTTCTAGTT AACTCATGTA AACAAGTAAG 1800
AGTAACATAA CAGTATTACC CTTTCACTGT TCTCACAGGA CATGTACCTA ATTATGGTAC 1860
TTATTTATGT AGTCACTGTA TTTCTGGATT TTTAAATTAA TAAAAAAGTT AATTTTGAAG 1920
AATCAAAAAA AAAAAAATAA AAAGTCGACC GGCAGCGAAT TTAGTAGTAG TAGTAGTAGT 1980
AGTAGGC

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1987

09646569 092000

(2) INFORMATION ON SEQ ID NO. 163:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1107 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```

GGGCCGGGCA GCCCAGCTGA AGGCAATAAG CTGGGCTCAC CGCTGCAGCA GAGTTCTGTG 60
CTAGCCGGGC ATAGGGGCGA GAGAAGGCCC AGAGGCGACG TCAGAGAGAA GCAACTGCGC 120
CCCGGTGAAG AGAAGCTCGC CCATCACCGG CTGGGAGCCA GCTTTCAGTG AAGATGGCAG 180
GGCCAGAACT GTTGCTTGAC TCCAACATCT GCCTCTGGGT GGTCCCTACCC ATCGTTATCA 240
CTCTTCGTAG ACATGATCCG CCACTACGTG TCCATCCTGC TGGAGAGCGA CAAGAAGCTC 300
ACCCAGGAAC AAGTATCTGA CAGGGGACGA GGCACCCACA GTCCCTCTCC CATAAGCCTG 360
CCAAGAAGAT TGATGTGGCC CGTGTAACGT TTGATCTGTA CAAGCTGAAC CCACAGGACT 420
TCATTGGCTG CCTGAACGTG AAGGCGACTT TTTATGATAC ATACTCCCTT TCCTATGATC 480
TGCACTGCTG TGGGGCCAAG CGCATCATGA AGGAAGCTTT CCGCTGGGCC CTCTTCAGCA 540
TGCAAGCCAC AGGCCACGTA CTGCTTGCCA CCTCCTGTTA CCTGCAGCAG CTCTTCGATG 600
CTACGGAGGA AGGGCAGCCC CCAAGGGGCA AGGCCTCATC CCTTATCCCG ACCTGTCTGA 660
AGATACTGCA GTGAAAGCCC AAGTCCTTGG AAGCTTTCCC CAGTGAAGGA CTGACTGGGG 720
GCCTCACGCT TAACTGGTAG TGCCACAAG CCTGGCAGCT GTAGAGCCGC GAACCTCCCC 780
ACACCTCCCT CACCGCGCAG GACCCTGAGT GAGGAGGAGG AGCTGGAAAC CTGGGGTGGG 840
TTGGCCAAAG GAGAACCCTA AGCTCCTGGC CTGATCCAGC TCCTTCCTGC CCAAGGCAGC 900
TTAGCCCATC CAGACTGGTC CTGAAGTCTG TCCCTCCATT GGCATGAAGT CTGCCCCTTA 960
GCAATCCGGC CTCGCAGGCT GTACTTTCAT GGTGCTCTCT ACCTTCTGGC CCCCATCCCG1020
GAACATTCCCT GAGTGAATTC GCAAGCGCAC TAGCATGTGA TATTAGGGAG TTTGCAATAA1080

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ATTATTGAGG CTGATGTAAA AAAAAAA

1107

(2) INFORMATION ON SEQ ID NO. 164:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1062 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GTGAATATGT GTGTATATGT GTGTGTATGT GTGTGTGGGG TTTGGGGTAG AAGGGAGGGA 60
 GGGGGCAGGA CAGTGTGGAA TCTCTAGGGT GTATGGGTAG GTAGGGGGCA CAGTTAGTTC 120
 TAAGTGGGCT TTTATGCTAA AAGCCTCTGG GGATATCTGT TTTGAAAATA AAGATAGGTG 180
 TCCCCTCCTT GCTGTCATCT AGCCAGACA CTCTGCTTGC TCTCTGGCTG TCTGCTCCCT 240
 GGGGAAGGCTT TAGGAGGACC ACCCAGGACA GGATGACCAT GCTGCCATCT GCTCTGGAGC 300
 TGGGTCTCAG TGCAGAGGGA CAGTACTGT GGATGGTTGC AGTCTCTGGT GGGAGGTGAG 360
 GATAGAAGTG ATAAAGAGCT AAGAGGAGCT TCTGGGAGCC TTGGAGGAGG TCAGTCTTGC 420
 AGTGGTGAAG CCAGGACATA GGAGATGGAG CAGGGCTGTG AGAGGAGGAG ATTCTGAGGA 480
 GGATGCAGGG GAAATCTTGT CTGTTAATGA AATAGGGGTG GGGTGGGGTT TGGGGTGGGG 540
 TGGTCATTGC CGTTTGAGCT GCTGATTTTC ATGAGTCGCC TTCAAACTC TCGTGTAGGG 600
 TTGACAATGT GGGGGGGTGG GGGATCCAGC TTATTCTTTT ATTTTCAAGT CCATTCTTGG 660
 GGCTGGTGGG GAGGCAGGAG AATACCCCTC CCTAAGCCCT TAGTGTGTGC CGAGCTTGCT 720
 TTGTGATGTT GGCAGGGGAG GGGAGACCTG GGTGGTGA CTGAGTCCCTT TATCAAACCC 780
 TTCAATGGGC ACAAATTGA GTGCTTGATT TTAGGTTTTA TTTTATTATG AATGTCCAAA 840
 TCTGTGTTTC CCCCTGCCCT CCCAGACTGT GTGGCCAGTT GAAAGTGTCT GGTGTGTGTT 900
 CATCTCTCCC TCATTCTTGG AGCAGGGCCT GAGACCTGC CACATCTCCT ATGCTCTGCA 960
 TCCACGCCTC TTTTGGACAT TAAAGGTTGA TTGATGCAAA AAAAAAATAC AACGGGGTGG 1020
 CTTGGGGAAG CCTGGGGTTG GCCGGCTTAT GGGGTGCGG CG 1062

(2) INFORMATION ON SEQ ID NO. 165:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 2770 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

09646569 "092000

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CTACTATGGA TAATTTCAAA GTAGAATCAC TCTATGCTTA GAGTTTTGGC ACCAATGCTG 60
 TAGGGCAGCA GAATCTATTC TCAGTAAAAT AACTTATGGT TTATTAGATA TTCTGTATTG 120
 GATTTTACCA GCTTGACTTT TACTGCTCAG ATGCTTTCTT TCCCCCCTT AGACGCTGTA 180
 ATTCTCTTGG GAAGAGTAAC TATTCTTAAG GTTTTACAG ATACCCACCT TAGTTGTAAA 240
 TTGGATAGTT TATATTTCTG GGACTTTTTA AATGAAAATG TGAATGTTA AGTTACAAAA 300
 GACTTTTCAT CAGAAAATTT CAAACAAAGT AAACATGGCG TTTTATAGTC CTCTAAAATC 360
 TAGGTGCTCC CACCCACCAA AGGCATATCC TGCAAAGGGC TGTGAACTAT CTTGGTGAAC 420
 TGTCTTGGGT CCCCTTTCCA TGTATGTTTT CTTGTCCTG AAAACAAACA ACGCTGAGTT 480
 TATCAAGAAA ATTTAAATTG GGGGATCATA ATAATTCCAA CCAAGTGACA ACTCTGACAT 540
 CAAGGTATT AGGAGCTGTA CATCCAATTC AAGTTTTATT TGCTGCTATT CTGGGAGAAT 600
 AAACCTGTAT ATGGAGAATA AACTAATAAA CTTGTATCGA GGAAATCCAT AAAGTTATAA 660
 ATTAGCCTGA AAAATATTTT AGGTAATGGT GTGGATTGGC CTGCTTTGAC TCTCAGCCAC 720
 CAACAGAAAT CTTTGTCAAC TTTGTTCCTC AGCTAAAAGT AATTTTGTTA TAAACACAAA 780
 GTGACTTTAA ACAGGTAAAA AACCCATTCC TATTTTTGTA CATTACCAA AGTTTTTCAT 840
 ATACCTACAG AGCTAACTAA TTACAACCTGA TTTAATCCAC TCAAGTTTAG ACCAGTTAAA 900
 CCCATAGGAT CCTGTATGGT TATCAATGTG ATGCCTTGCT TTTTATAAAA TAGGTATAAT 960
 TGGGTCATAC ACTTGACGAG AGGGTGACTG TTTCTAGGGG AAGAAAACCC TTTAGATTGC1020
 AGGTAACCTT CACTTTTTTT TTTTTAAATA TACACTTTAC ATTTGTATAA ATTATGCAGG1080
 GTACTCCTAA CCCTGTAGAA ATGTATGACC TCTCACAAG TTGAGATTTG ATCCAAAGAG1140
 AAATGCAAGT ATAAAAGAAT TAGATACCTT ATTATCTTTT AAGGTTTTTT TTTTTTTTG1200
 GTAGAGATGG GGGTCTCACT GTGTTGCCCA GGCTGGTCTC AAACCTCTGG CCACAAGTGA1260
 TCTTCCTGCC TCAGCCTCCC AAAATGCTGA GATTACAGGC ATGAGCCACT GTACCCAGCC1320
 TTTCTTATA AAATTCAAAG AGAAAATTTT TACACCTTTA TCCCTCAAAT AAAACAAGTG1380
 CTCAGTTCTT ACCGTGCCCT TGCAAGGTCT ATATGTAAAA GAAATCTGAA ATTTAGCTGT1440
 AGAATAAAAC TTGATAAATA AAAAGAAAAA ACATACATTT CTCCAGTTGG TTTGCTCTTT1500
 GCTTGTTGAA GTAATAAACC GTTTTAAAGA GAAAATACTT GCTGTAAACC CCCAGTGCCT1560
 TCAACTCTTT TGGCAGAATA TTTTAAAGA AATCCAGCAA GCAAACCTTG AGGTGCTAAT1620
 GAAAGTAAAG GAAGGTGGTA TTTCTAGTTT TGGCAGAAAT GAAAAGTGTC TCACAAGAGA1680
 CATCACTACC CACGTGGGGT CTGGCTGCTT TCTACCAAAG ACATTTAGAG AAGAAGTGAA1740
 TTGAGTCAGG GTGATGGTGA AACTACATA TTTTATAGAT GGTTAAGTTG AGAATTAATT1800

ATGTTTATCA TGGATGGCTA CTAATACCAA GCTCATGATT GTTGCAAGCT CAACGTCTTA1860
 GGCAGTAAAA CTTGTCTGCA GCACTAAAGG GGGAGAAACC CTTATATTTT GCAAACTGTC1920
 CATTGCTTAA ATTTATTGTA ACCTAATACC AAAAAGTCC GTTTTTCATA TTATTTCCCC1980
 ACCTCCTACT TTTTTGTTT TTTTTGCTA CTTGTAAAT AACCCTTCT AGAAAATAAG2040
 CATTAACTGG AATGTTTCAA ACAATTTTGC TTCATTTTAC TATCAGCCAC TAGTGAAGTCT2100
 TTACAGAGAT GTACATTTAA GATAAAATTA GCTTGTGCTA AGTGTTTTAA AAACATTGTT2160
 TACTGTTAAA GGGGAATTGC ACATTATATT TAAGTGGAT TGCTCCCTCC CTCAGTTCTT2220
 TAAAAACAA GAGTCAAGGC TCACACCAAC TTGTAGGCTG TGGGAGCTTT GCCATAGGTA2280
 GATACAATGT AGAAGTATAC TTTTTTAAAG CATGAAGAAG ACAAGGAAGT TCATTATAAT2340
 GTACCAGGTA GAGGACATTA TTATTCAAAG GATTATGCAC AGCTCAGTGA AGATGAAGTT2400
 ACAATTTTTC TCGCAGCTTT GTTGCTATTA TTTTCTTCTG CATAAATGTA TGCTCATTTT2460
 ATTATGTGCC TTGCTCCCTG ATTGTGCAAA GCTATATATA TATATATATA TATAGATAGA2520
 TAGATAGATA GATATATGAG AGAGATATAT TCAGTACTAC TGAGGATGTT TTTCTGAGGA2580
 TGTTTTTGTT CTGCTGGATT AAGTTATTTT CCAAGTTACT CTTGCCAGTT ATGTCAGTAA2640
 ACTATTGTAA TGGCTTAGCA CACTAGTCGT ACAGTCAGTG TAAATGTTTT TCATTTACAT2700
 GTTTTCATTA TATCAGCTTA TCAAATCCTT AATAAAAAAA ATTCATAGAT TTCATTTAAA2760
 CAAAAA

2770

0064559 "092000

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 4242 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

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GGCCATTGAC CCTAGAGGTG AAACCGAAGC TCTGATGGAC TCTCACAGCT GGAGATGAAA 60
ATACGAGTTA TACACGGAGA ATGCAACCAC TGAGAAAACG GAACCGAATA GTCAAGAGGA 120
CAAGAATGAT GGTGGAAAAT CAAGAAAAGG GAATATAGAA CTTGCCTCAT CAGAACCACA 180
GCATTTTACA ACAAAGTGTG CTGATGCAG CCCGACCGTG GCCTTTGTGG AATTTCCCTC 240
CAGCCCCCAG CTGAAGAATG ATGTGTCGGA AGAAAAAGAC CAGAAGAAAC CAGAAAATGA 300
AATGAGTGGA AAGGTGGAGT TGGTGCTGTC ACAAAGGTG GTAAAGCCAA AATCTCCAGA 360
ACCGAAGCA ACGCTGACAT TTCCATTCTT GGACAAAATG CCTGAAGCCA ACCAACTACA 420
TTTGCCAAAT CTCAATTCTC AAGTGGATTC TCCAAGCAGT GAGAAGTCAC CTGTTATGAC 480
ACCTTTTAAG TTCTGGGCAT GGGACCCAGA AGAGGAGCGC AGGCGACAGG AAAAATGGCA 540

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09646569.092000

ACAGGAACAG	GAACGTTTGC	TCCAGGAGAG	ATACCAGAAG	GAGCAGGACA	AGCTGAAAGA	600
AGAGTGGGAA	AAGGCCCAAA	AGGAGGTGGA	AGAGGAAGAA	CGCAGATACT	ATGAGGAGGA	660
GCGTAAGATA	ATTGAAGACA	CTGTGGTTCC	ATTTACTGTT	TCTTCAAGTT	CCGCTGACCA	720
GCTGTCTACC	TCTTCTCCA	TGACTGAAGG	CAGTGGGACA	ATGAATAAGA	TAGACCTGGG	780
AAACTGTCAA	GATGAAAAAC	AAGACAGAAG	ATGGAAGAAA	TCATTCCAGG	GAGATGACAG	840
TGACTTATTG	CTGAAGACTA	GGGAAAAGTA	TCGACTGGAG	GAGAAGGGCA	GCCTAACTGA	900
AGGGGCCCTT	GCTCATTCTG	GGAACCCGTG	ATCAAAAAGGA	GTCCATGAAG	ACCATCAGCT	960
GGATACCGAG	GCTGGGGCCC	CACACTGTGG	AACAAACCCA	CAGCTTGCTC	AGGATCCATC	1020
CCAGAATCAG	CAGACATCAA	ATCCAACGCA	CAGTTCAGAA	GATGTGAAGC	CAAAAACCCCT	1080
CCCGCTGGAT	AAAAGCATTA	ACCATCAGAT	CGAGTCTCCC	AGTGAAAGGC	GGAAGTCTAT	1140
AAGTGGAAAG	AAGCTGTGCT	CTTCTGTGGG	GCTTCTTTTG	GGTAAAGGAG	CTGCAATGAT	1200
CATCGAGACC	CTCAATCTCT	ATTTTCACAT	CCAGTGTGTT	AGGTGTGGAA	TTTGTAAGG	1260
CCAGCTTGGA	GATGCAGTGA	GTGGGACGGA	TGTTAGGATT	CGAAATGGTC	TCTGAACTG	1320
TAATGATTGC	TACATGCGAT	CCAGAAGTGC	CGGGCAGCCT	ACAACATTGT	GACACGGCTT	1380
TCAAGCTTCC	GGATCACTCA	CCATTTCTTT	ACTGAGAGTG	TCCCCTGGCA	ACTGCTTAAC	1440
AAAATCCCAA	GCTCAGGGGC	TTCTCAGCAT	TTACCTAATT	TCTGAAAGGC	TCTTCTGAAA	1500
GGTGGTATCT	GTTCTTTTCG	AGCACAGTGT	TTATGTTTTT	CCTGTTTTATT	GTTTTGGGTT	1560
TTTGTTTTTT	TTTTTGCAAT	TGCACAGTAT	ACACAAAAGA	ATATGGGGTT	GTAATGATCC	1620
TGAATAGCTC	AAAAAAGGTT	TTAGCATGGT	CAAACAGGCT	TATGGTTTTAA	AATGTGTTAT	1680
TCTCTTCTTT	GGGAATTAGC	TAAATGATGC	AATAAACCTG	TTTTGTTTTA	GAATGTCTAG	1740
GAATTAACA	CTTTATGTTT	ACAGAATTGA	GCTGCAGAAA	GTGCAAGACA	TGCCAATTTG	1800
AGACACACGG	TCTTCTAAGA	CTAAGGATA	AATTTAATGC	ATTTCAGAAA	CTAAACATCA	1860
CAGCAAGCTC	TATCTCTGAG	CTATAATTG	TTTTTAATGC	AAAGACATA	GTTTGATAAT	1920
ATATACTGTA	ATCCTGAAAC	ATTTGTGTTA	CTTACCTTTG	GAGGTAGAAA	TTATACCAAT	1980
AAATTATTGC	ACCGTTAGTA	TTAGATTCTG	TGTACCTTGG	AAGTTATGTC	ATTAATATAG	2040
GCTGGTTCAT	CAAATAAAGC	AAAACCTTGC	AATATCAGCT	AGATTTACAC	TCCGGGACGT	2100
TGCCCAAAGG	TAGGAAGAAA	GCAGAGGGAA	ATATTTCACT	CATCATTTCC	AAAGTCATTA	2160
TCAAAATCTG	TGAGGAAGTT	TAATCTTCCA	AAGAGTCAAT	GTCAGACATC	AGGCCTCTGT	2220
TGCCCTGCTC	TCTCGAGGCA	CTAGATTAGG	AGTCTTCAAT	AAGAGACTTA	ACATGAGGTA	2280
TATGGAAGAT	GAGGCACCGA	GATAAGTTCA	TCATTAGGTG	TGAGCACTGC	TCACCCTTGC	2340
TGGCAAGTTC	TCCTTAAGGG	CCTGAAGCAC	AGGTGTCCAA	AGAAAAGCGT	TAAGTCCATC	2400
TTAATAGAA	CTTATGGGTA	TATGACTGTG	TCAGCCCCTG	GTCTGTGATC	AGCAAGAACC	2460
TACAGCACAG	ATTATGCCCT	GCCCACTTCA	ATGAATACCT	ACTCTCTCTC	ATTCTCCATC	2520
ACTTTTTTTT	CTATCAAGAA	CTCCGGACCT	TGCCCATGGA	GAAGTTTAGA	GAGGAACTCT	2580
TGTGGAGAGC	TGGTTTATTT	TCTGCCCTGT	GCGACGAGTT	TCAGCTGGCC	AAGAAAGGAG	2640
TCAAGTTATT	AAAAAGCATC	ACAATGTAGA	TCTCCAGGCT	GGTTTTTTGT	TTTTTGTTGT	2700
TAAGACTGGG	GAAAGGGGGA	CTATTTATTC	TGCCTTAAAT	CAATGGCAAA	TAAGTCAAGA	2760
TGACATTTTG	TGAATGTAGA	CTATGGATAC	ACTCCTAATA	GATTGATGTA	GTCATAAAAG	2820
GGGGTCAAGT	AGATGTTTTT	CTGTTATGTA	AGCAATAATT	TTTCCGTGTC	TTATTGAGTA	2880
TGGCTATCGA	TTATTTATTA	CATGCTAGAT	GGGTTCTTTG	CATGTGGGTT	CCATATAGGT	2940
GCGAAAATTT	CCTCAGCCAC	TGGAGGGATT	TCGACCATAT	TTGTCATTTG	GATGAGCTGT	3000
TATTAGATTG	AAATCTACAC	ATCATTTTAT	TAAAAATTGT	GCCTTAGAAA	ACGCAAAGCT	3060
GTTGCACATG	GCGATAAATT	ATGATGTCAG	TACATTGAAG	AGAGATGAAG	TCACTTCCAA	3120
GTTTCCAAGA	CTTCTCATGG	AGGTGTTTTG	TGTTTTACAG	GAAAAAATAA	AAATAAAAAA	3180
AGAAAAAAAT	GAGAAAAAAT	TAAATTCAAA	AATTGTTTTG	AAAATGTACA	GATCAAGTCC	3240
AATATTTTGA	TTATCCACCT	GCATGTTTTA	TTAAATATTT	TGATAATGTG	GATGTTTACA	3300
CTTTGCATGA	TATTAGCAGA	GTACCACTAG	TAATGCACAA	ACATGTACAA	TATGGTCATT	3360
CATAACCGAT	TTTTATAGAA	TACTTTTTTAC	ATGTGCAACT	CCATCCGTTA	TGTAAGGATT	3420
ACATGAATAT	TGCACATTCC	CTTCTGGTTT	CACAAACCCA	TTTATACATA	TTTCTTAGTG	3480
AGGCTCATTG	TACATGTATT	GAAGCTAGAA	TCGAGTCAAG	AAAAATAAAG	CCCCATTCTC	3540
CAACTGCAAA	ATGTGCTTTT	CCATAATGAA	CACTAGTCAC	CAGCACAGAA	TAATCTCCAA	3600
CATTTTCTAA	ATTCTAATTG	CCAAGCTGTT	CTATTTATAT	TTGATTTATA	TTTCATTGGG	3660
AGTCTGTTAC	ATGGCAGCTT	AGGCAGACTA	GATCTTGTTT	TTTCCAATGC	AGCATAATGA	3720
GTATGATCTA	TTTCTTTTCA	AATAATCTTT	GAGATCCCAG	GAAAAAAAAT	ATGCTCTGCT	3780
CCATTGAGCT	ATAATGTAAA	TGTGTTTGTT	TAAAAAACAG	GTGAGGCAAG	TGAGTGATTT	3840
ATTGTTTCTG	AGGAAGTATA	TCTGATTTTT	TTTCTCATAC	TCCAAAAGCT	AGTCCCTACT	3900

(2) INFORMATION ON SEQ ID NO. 167:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CTAGCAAGCA	GGTAAACGAG	CTTTGTACAA	ACACACACAG	ACCAACACAT	CCGGGGATGG	60
CTGTGTGTTG	CTAGAGCAGA	GGCTGATTAA	ACACTCAGTG	TGTTGGCTCT	CTGTGCCACT	120
CCTGAAAAAT	AATGAATTGG	GTAAGGAACA	GTTAATAAGA	AAATGTGCCT	TGCTAACTGT	180
GCACATTACA	ACAAAGAGCT	GGCAGCTCCT	GAAGGAAAAG	GGCTTGTGCC	GCTGCCGTTT	240
AAACTTGTCA	GTCAACTCAT	GCCAGCAGCC	TCAGCGTCTG	CCTCCCCAGC	ACCTCCCTCAT	300
TACTGTGTCT	TGTCTGGCCT	GATCTGTGCA	TCTGCTCGGA	GACGCTCCTG	ACAAGTCGGG	360
AATTTCTCTA	TTTCTCCACT	GGTGCAAAGA	GCGGATTTCT	CCCTGCTTCT	CTTCTGTCAC	420
CCCCGCTCCT	CTCCCCCAGG	AGGCTCCTTG	ATTTATGGTA	GCTTTGGACT	TGCTTCCCCG	480
TCTGACTGTC	CTTGACTTCT	AGAATCGAAG	AAGCTGAGCT	GGTGAAGGGA	AGACTCCAGG	540
CCATCACAGA	TAAAAGAAAA	ATACAGGAAG	AAATCTCACA	GAAGCGTCTG	AAAATAGAGG	600
AAGACAAACT	AAAGCACCAG	CATTTGAAGA	AAAAGGCCTT	GAGGGAGAAA	TGGCTTCTAG	660
ATGGAATCAG	CAGCGGAAAA	GAACAGGAAG	AGATGAAGAA	GCAAAATCAA	CAAGACCAGC	720
ACCAGATCCA	GGTTCTAGAA	CAAAGTATCC	TCAGGCTTGA	GAAAGAGATC	CAAGATCTTG	780
AAAAGCTGA	ACTGCAAATC	TCAACGAAGG	AAGAGGCCAT	TTTAAAGAAA	CTAAAGTCAA	840
TTGAGCGGAC	AACGAAGAC	ATTATAAGAT	CTGTGAAAGT	GGAAAGAGAA	GAAAGAGCAG	900
AAGAGTCAAT	TGAGGACATC	TATGCTAATA	TCCTGACCT	TCCAAAGTCC	TACATACCTT	960
CTAGGTTAAG	GAAGGAGATA	AATGAAGAAA	AAGAAGATGA	TGAACAAAAT	AGGAAAGCTT	1020
TATATGCCAT	GGAAATTTAA	GTTGAAAAAG	ACTTGAAGAC	TGGAGAAAGT	ACAGTTCTGT	1080
CTTCCAATAC	CTCTGGCCAT	CAGATGACTT	TAAAAGGTAC	AGGAGTAAAA	GTTTAAGATC	1140
ATGGGCAAAA	GTCCAGTGTA	TTCAGTAAAG	TGCTAATCAC	AAGTTGGAGG	TCAATGGCAG	1200
CGATGGCCTG	GCACCAAGTTG	AAGTAGAGGA	ACTTCTAAGA	CAAGCCTCAG	AGAGAAACTC	1260

TAAATCCCCA ACAGAGTATC ATGAGCCTGT ATATGCCAAT CCCTTTTACA GGCCTACAAC1320
 CCCACAGAGA GAAACGGTGA CCCCTGGACC AAACCTTTCAA GAAAGGATAA AGATTAAAAC1380
 TAATGGACTG GGTATTGGTG TAAATGAATC CATAACAAT ATGGGCAATG GTCTTTCAGA1440
 GGAAAGGGGA AACAACCTCA ATCACATCAG TCCCATTCCG CCAGTGCCTC ATCCCCGATC1500
 AGTGATTCAA CAAGCAGAAAG AGAAGCTTCA CACCCCGCAA AAAAGGCTAA TGAATCCTT31560
 GGAAGAATCG AATGTCATGC AGGACAAAGA TGCACCCTCT CCAAAGCCAA GGCTGAGCCC1620
 CAGAGAGACA ATATTTGGGA AATCTGAACA CCAGAATTCT TCACCCACTT GTCAGGAGGA1680
 CGAGGAAGAT GTCAGATATA ATATCGTTCA TTCCCTGCCT CCAGACATAA ATGATACAGA1740
 ACCGGTGACA ATGATTTTCA TGGGGTATCA GCAGGCAGAA GACAGTGAAG AAGATAAGAA1800
 GTTTCTGACA GGATATGATG GGATCATCCA TGCTGAGCTG GTTGTGATTG ATGATGAGGA1860
 GGAGGAGGAT GAAGGAGAAG CAGAGAAACC GTCCTACCAC CCCATAGCTC CCCATAGTCA1920
 GGTGTACCAG CCAGCCAAAC CAACACCACT TCCTAGAAAA AGATCAGAAG CTAGTCCTCA1980
 TGAAAACACA AATCATAAAT CCCCCACAA AAATTCCATA TCTCTGAAAG AGCAAGAAGA2040
 AAGCTTAGGC AGCCCTGTCC ACCATTCCCC ATTTGATGCT CAGACAACCTG GAGATGGGAC2100
 TGAGGATCCA TCCTTAACAG CTTTAAGGAT GAGAATGGCA AAGCTGGGAA AAAAGGTGAT2160
 CTAAGAGTTG TACCACCTAT ATAAACATCC TTTGAAGAAG AAACCTAAGAA GCATTTGCAA2220
 ATTTCTCTTC TGGATATTTT GTTTATTTTT TCTGAAGTCC AAAAAATTAT CATTACAGTG2280
 TACCATATTA AGCCATGTGA ATAAGTAGTA GTCATTATTT GTGAAAAATT CCCAAAAAGC2340
 TGGGGAAAAC AAATGTGTAA CTTTCCAGT TACTTGACAC GATTCACTGG GGGAAAACCA2400
 GCATTTTTTA TTCTATTGAT ACCAAAGCAT TTCTAATAAG AGCTTGTTAA ATTTAAGAAT2460
 AAAGTTATTT AAAATATTCT GAGTATAGTA TATTAACCTG CATTGTAATT TTGATGATAC2520
 AAAGATTGAA AGATCATAGG AAAGCATTGC CTTTCATCAC AGAAGTATTC AACTCTGACA2580
 AATAAATATG TCATCCTGAA TTAATAATGC CTTAATAAAA GTACATCCTC CTGCTAAAAA2640

(2) INFORMATION ON SEQ ID NO. 168:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1558 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260"69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GCGAGGAGCT GGCACGCAGC CAGGGCCTTT GCTCAAGAAG CCATACCAGC CAAGAATTAA 60
 AATCTCTAAA ACATCAGTGG ATGGTGATCC CCACTTTGTT GTGGATTTC CCCTGAGCAG 120
 ACTCACCGTG TGCTTCAACA TTGATGGGCA GCCCGGGGAC ATCCTCAGGC TGGTCTCTGA 180

 TCACAGGGAC TCTGGTGTCA CAGTGAACGG AGAGTTAATT GGGGCACCCG CCCCTCCAAA 240
 TGGCCACAAG AAACAGCGCA CTTACTTGCG CACTATCACC ATCCTCATCA ACAAGCCAGA 300
 GAGATCTTAT CTCGAGATCA CACCGAGCAG AGTCATCTTG GATGGTGGGG ACAGACTGGT 360
 GCTCCCCTGC AACCAGAGTG TGGTGGTGGG GAGCTGGGGG CTGGAGGTGT CCGTGTCTGC 420
 CAACGCCAAT GTCACCGTCA CCATCCAGGG CTCCATAGCC TTTGTCATCC TCATCCACCT 480
 CTACAAAAAG CCGGCGCCCT TCCAGCGACA CCACCTGGGT TTCTACATTG CCAACAGCGA 540
 GGGCCTTTCC AGCAACTGCC ACGGACTGCT GGGTCAGTTC CTGAATCAGG ATGCCAGACT 600
 CACAGAAGAC CCTGCAGGGC CCAGCCAGAA CCTCACTCAC CCTCTGCTCC TTCAGGTGGG 660
 AGAGGGGCTT GAGGCCGTCC TAACAGTGAA AGGCCACCAA GTCCCAGTGG TCTGGAAGCA 720
 AAGGAAGATT TACAACGGGG AAGAGCAGAT AGACTGCTGG TTTGCCAGGA ACAATGCCGC 780
 CAAACTGATT GACGGGGAGT ACAAGGATTA CCTGGCATCC CATCCATTTC ACACAGGGAT 840
 GACACTTGGC CAGGGAATGT CCAGGGAGCT CTGAAGCTGG CAGCCTTAAA GATGCAAGTG 900
 CATGAAGGAC AGTGATGTGG GGAGGCCGTG ACCCACCCTT TTTTCATGGCT TGTACACGCC 960
 TCAGCTCCTG GCAATTAGCT GGACTCCATG ACCCACCCTT GGTGCAGCAT AGATCCGACG 1020
 TCTGTCTGGG CGAAGGGTAG GGGTGGGTAG GGGCGGGAAG CCTGAGTGCA AATGTCATTT 1080
 CCCTCTACTG CCTCTTCCTG CCTCTCCCCA CCCTGCCCAC ATCCACAGAG GGGAGAGAAG 1140
 GGTCATAGCT AAATGCAACA AAGTCTGTAT CTTGTCCCAA CCTGCTTTTC TGTTCCTGTTA 1200
 GCATATCATA AAGTAAGCCT TTCTGGTGAA GGAAGGTTGC TATGAAACTT TTTTCTTGG 1260
 TGGAAATGGC CAAGTTTAGG CACTCTGCTT TTTGCCCTAC ACTAATGCTT AGAAAGCTGT 1320
 CTTTTAGTGT GTGTTGCAGC CCCCAGATGT GTGGCCAAAC TCTGCTGCAA AGGAATCTCT 1380
 TGCTGAGTCC AGGCCACCAA TCAGGCAAAT AGCCCATACA TTTGATCGTT GTAAACCATG 1440
 AAGTCTTTTC TTGCAAGACG TTTTCTTCT GCTGTGGTAT CTTGCCCTTA AAAATTAGTT 1500
 TTCATTAAAA AGAAATTTGA TTGAAAATAA AAAACCGGAA TGGAAAAAAA ATTGTTTT 1558

(2) INFORMATION ON SEQ ID NO. 169:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1388 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

00020"0954569"092000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

CGGGGGTTCAC TGTGTTGGCC AGGCTGGTCT CGAACTCCTG ACCTCATGAT CTGCCCCGCCT 60
 CAGCCTCCCA AAGTGCTGGG ATTACAAGTG TGAGCCACCA CACCTGGCCT GGAAGGAACC 120
 TCTTAAAATC AGTTTACGTC TTGTATTTTG TTCTGTGATG GAGGACACTG GAGAGAGTTG 180

CTATTCCAGT CAATCATGTC GAGTCACTGG ACTCTGAAAA TCCTATTGGT TCCTTTATTT 240
 TATTTGAGTT TAGAGTTCCC TTCTGGGTTT GTATTATGTC TGGCAAATGA CCTGGGTTAT 300
 CACTTTTCCT CCAGGGTTAG ATCATAGATC TTGGAAACTC CTTAGAGAGC ATTTTGCTCC 360
 TACCAAGGAT CAGATACTGG AGCCCCACAT AATAGATTTT ATTTCACTCT AGCCTACATA 420
 GAGCTTTCTG TTGCTGTCTC TTGCCATGCA CTTGTGCGGT GATTACACAC TTGACAGTAC 480
 CAGGAGACAA ATGACTTACA GATCCCCCGA CATGCCTCTT CCCCTTGGCA AGCTCAGTTG 540
 CCCTGATAGT AGCACGTTTC TGTTTCTGAT GTACCTTTTT TCTCTTCTT TTTGCATCAG 600
 CCAATTCCCA GAATTTCCCC AGGCAATTTG TAGAGGACCT TTTTGGGGTC CTATATGAGC 660
 CATGTCCTCA AAGCTTTTAA ACCTCCTTGC TCTCCTACAA TATTCAGTAC ATGACCACTG 720
 TCATCCTAGA AGGCTTCTGA AAAGAGGGGC AAGAGCCACT CTGCGCCACA AAGGTTGGGT 780
 CCATCTTCTC TCCGAGGTTG TGAAAGTTTT CAAATTGTAC TAATAGGCTG GGGCCCTGAC 840
 TTGGCTGTGG GCTTTGGGAG GGGTAAGCTG CTTTCTAGAT CTCTCCCAGT GAGGCATGGA 900
 GGTGTTTCTG AATTTTGTCT ACCTCACAGG GATGTTGTGA GGCTTGAAAA GGTCAAAAAA 960
 TGATGGCCCC TTGAGCTCTT TGTAAGAAAG GTAGATGAAA TATCGGATGT AATCTGAAAA1020
 AAAGATAAAA TGTGACTTCC CCTGCTCTGT GCAGCAGTCG GGCTGGATGC TCTGTGGCCT1080
 TTCTTGGGTC CTCATGCCAC CCCACAGCTC CAGGAACCTT GAAGCCAATC TGGGGGACTT1140
 TCAGATGTTT GACAAAGAGG TACCAGGCAA ACTTCCTGCT ACACATGCCC TGAATGAATT1200
 GCTAAATTTT AAAGGAAATG GACCCTGCTT TTAAGGATGT ACAAAGTAT GTCTGCATCG1260
 ATGTCTGTAC TGTAATTTT TAATTTATCA CTGTACAAAG AAAACCCCTT GCTATTTAAT1320
 TTTGTATTAA AGGAAAATAA AGTTTTGTTT GTTAAAAAAA AAAAAAAAAA AAAAAAAAAA1380
 AAAAAAAA 1388

(2) INFORMATION ON SEQ ID NO. 170:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2416 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GTCCCTGGCG CCCTGCCTTT AGCCGTGGGG CCCCCACCTC CACCCTCTGG GTTTCCTAGG 60
 AATGTCCAGC CTCGGAGACC TTCACAAAGC CTTGGGAGGG TGATGAGTGC TGGTCTTGAC 120

AAGAGGCCGC TGGGGACACT GTGCTGTTTT GTTTCGTTTT TGTGATCTCC CGGCACGTTT 180
 GGAGCTGGGA AGACCACACT GGTGGCAGAA TCCTAAAATT AAAGGAGGCA GGCTCCTAGT 240
 TGCTGAAAGT TAAGGAATGT GTAAAACCTC CACGTGACTG TTTGGTGCAT CTTGACCTGG 300
 GAAGACGCCT CATGGGAACG AACTTGGACA GGTGTTGGGT TGAGGCCTCT TCTGCAGGAA 360
 GTCCCTGAGC TGAGACGCAA GTTGGCTGGG TGGTCCACAC CCTGGCTCTC CTGCAGGTCC 420
 ACACACCTTC CAGGCCTGTG GCCTGCCTCC AAAGATGTGC AAGGGCAGGC TGGCTGCACG 480
 GGGAGAGGGA AGTATTTTGC CGAAATATGA GAACTGGGGC CTCCTGCTCC CAGGGAGCTC 540
 CAGGGCCCCCT CTCTCCTCCC ACCTGGACTT GGGGGGAACT GAGAAACACT TTCCTGGAGC 600
 TGCTGGCTTT TGCACTTTTT TGATGGCAGA AGTGTGACCT GAGAGTCCCA CCTTCTCTTC 660
 AGGAACGTAG ATGTCGGGGT GTCTTGCCCT GGGGGGCTTG GAACCTCTGA AGGTGGGGAG 720
 CGGAACACCT GGCATCCTTC CCCAGCACTT GCATTACCGT CCCTGCTCTT CCCAGGTGGG 780
 GACAGTGGCC CAAGCAAGGC CTCACTCGCA GCCACTTCTT CAAGAGCTGC CTGCACACTG 840
 TCTTGAGCA TCTGCCTTGT GCCTGGCACT CTGCCGGTGC CTTGGGAAGG TCGGAAGAGT 900
 GGAACCTTGT CTGGCCTTCC CTTTCATGGCG TCTATGACAC TTTTGTGGTG ATGGAAAGCA 960
 TGGGACCTGT CGTCTCAGCC TGTTGGTTTT TCCTCATTGC CTCAAACCCT GGGGTAGGTG 1020
 GGACGGGGGG TCTCGTGCCC AGATGAAACC ATTTGGAAAC TCGGCAGCAG AGTTTGTCCA 1080
 AATGACCCTT TTCAGGATGT CTCAAAGCTT GTGCCAAAGG TCACTTTTCT TTCCTGCCTT 1140
 CTGCTGTGAG CCCTGAGATC CTCCTCCCAG CTCAAGGGAG AGGTCTGGG TGAGGGTGGG 1200
 AGATTTAGAC ACCTGAAACT GGGCGTGGAG AGAAGAGCCG TTGCTGTTTG TTTTTTGGGA 1260
 AGAGCTTTTA AAGAATGCAT GTTTTTTTTCC TGTTTGGAAAT TGAGTAGGAA CTGAGCTGT 1320
 GCTTCAGGTA TGGTACAATC AAGTGGGGGA TTTTCATGCT GAACCATTC AAGCCCTCCC 1380
 GCGCGTTGCA CCCACTTTGG CTGGCGTCTG CTGGAGAGGA TGTCTCTGTC CGCATTCCTC 1440
 TGCAGCTCCA GGCTCGCGCA GTTTTCTCTC TCTCCCTGGA TGTTGAGTCT CATCAGAATA 1500
 TGTGGGTAGG GGGTGGACGT GCACGGGTGC ATGATTGTGC TTAACCTGGT TGTATTTTTC 1560
 GATTTGACAT GGAAGGCCTG TTGCTTTGCT CTTGAGAATA GTTTCTCGTG TCCCCCTCGC 1620
 AGGCCTCATT CTTTGAACAT CAACTCTGAA GTTTGATACA GATAGGGGCT TGATAGCTGT 1680
 GGTCCCCTCT CCCCTCTGAC TACCTAAAAT CAATACCTAA ATACAGAAGC CTTGGTCTAA 1740
 CACGGGACTT TTAGTTTGGC AAGGGCCTAG ATAGGGAGAG AGGTAACATG AATCTGGACA 1800
 GGGAGGGGAG TACTATAGAA AGGAGAACAC TGCCTACTTT GCAAGCCAGT GACCTGCCTT 1860
 TTGAGGGGAC ATTGGACGGG GGCCGGGGGC GGGGGTTGGG TTTGAGCTAC AGTCATGAAC 1920
 TTTTGGCGTC TACTGATTCC TCCAACCTCT CACCCACAA AATAACGGGG ACCAATATTT 1980
 TTAACCTTGC CTATTTGTTT TTGGGTGAGT TTCCCCCTC CTTATTCTGT CCTGAGACCA 2040
 CGGGCAAAGC TCTTCATTTT GAGAGAGAAG AAAAACTGTT TGGAACCACA CCAATGATAT 2100
 TTTTCTTTGT AATACTTGAA ATTTATTTTT TTATTATTTT GATAGCAGAT GTGCTATTTA 2160
 TTTATTTAAT ATGTATAAGG AGCCTAAACA ATAGAAAGCT GTAGAGATTG GGTTCATTG 2220
 TTAATTGGTT TGGGAGCCTC CTATGTGTGA CTTATGACTT CTCTGTGTTT TGTGTATTTG 2280
 TCTGAATTAA TGACCTGGGA TATAAAGCTA TGCTAGCTTT CAAACAGGAG ATGCCTTTCA 2340
 GAAATTTGTA TATTTTGCAG TTGCCAGACC AATAAAATAC CTGTTTGAAA TACAAAAAAA 2400
 AAAAAAAAAA CTCGAG 2416

(2) INFORMATION ON SEQ ID NO. 171:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2720 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

000260" 69554960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGAGCTGTCC CTGACTNTGC AGGCCTGAGC GAGTGTGTGA GCATGCGGGG ACATGGGTGT 60
GTATGGCACA CATAGGTGCG TGTGTGTCTT TTGTATTTTT TCTCCTCCAA GGAGCTGTGT 120
CAGTGTGGAC GTTCTGTTTC AGGGAGTTGG AAAGGAGGGT GTCTGCAGAA GGTGGAGAGC 180
AGGGGCAGAG GCCCCACTGG CCACCCCTG CTTCCAGAG TGAAACCTTG TGCCTGGTGA 240
CCAAAGTCCC TCCAAAGTGC TCTTCCTTCT GGGTTATTCA AGCCAAATAT CTGGGTTTTCC 300
CCCTCTCCTC ATTCCCTAGC AAACCCCAAT TATCTTTCAA GATAGGAGAT ATTTCCCATC 360
CCCTTCCTTT GTAAATATCT CATCTCCCAC TGGAGAGCCC AGGAGCCTAT TCCTGGCATG 420
GATGTTCTGT CCACACTTGA GGCTGGGCGG TGTATCAGAC CCTTCAAGCA GCCTGGCTGG 480
GGCCAGGAC TGAGTCTGGG GTCAGCTTTC ACGGTCGCTT TTCCCTTCCT CACCACCCAC 540
CACAGCCCAC CTTGCATGCA TGGCCAGCCC CTCCACTCCA GCCTGAGCCA TGTGTGCCCC 600
TGCGGGAGGA CCCATTTCATG CCAGAAAGCT GGTAACCTCC TCCCAGCATC CCTGCGGAAG 660
GAGTCAGTTT CTGAGAGTGT GACTTTTCAA GGCGAATGAT GGGGAAGGGT TCCCCAGTCC 720
CCACAGTGGC CCCACCTCTG GGCCCTGCAC CAGAGCCCTT CTGTGTCACG GCGGGCTGTG 780
CACCCATGCA CACACCTACG CACACACAAC ACTCCGCACT GCAGTATATT CTTGCCAAAG 840
ATTTCTTTTA AAAGCAAGCA CTTTTACTAA TTATTATTTT GTAAATGTTT ATCTTCTTCT 900
GTCTTCTCCC TCCCTGAATC TATTTTACTG TTGTTTATTG TTGAATCTGT GTGTGAGCCA 960
GGAGAGCGCT GTCTGGCCTT GAACATGGGC TGGGATGGGA AAGGGTCTGG GAGAAGATGG1020
GCAACAAAGA GCCAGGGAGT CATGGACATC GCAGCGACGC AGACCCACAG AGGTTTCAGTC1080
CCGTGCTGCC ACCAGCTGTC CAGCTGGGTG TCTGGAGGGA AGAGGGCAGA GGAGGGTCAT1140
GTCCCTTCAG CTGGGGGAGG GGCCCACTGA GCTCCACGTG GCTTTTTCCC AAAGGGAGCA1200
AGAGGGAAGG ATTGGGCGAG AAAACAATGG AGAGGGGACC TGCGAAGGAA AACAGGGAGG1260
AAGTGAGCGG TTTGATCAGC CTGCTATCAC GGTGTTCTGG CTCTCTTATT TAGCCAGGCG1320
CTTAAGGGAC AGATACATCA CATCCTAAGT TTGGGAAAGG CCTTTGACCC ATGTCATCTG1380
AGCGTCTCCT CCACTAGCTC TGAAAGCTGT GGACACCAAT GGCCAGGATT CCTTCTCCCC1440
TGTTTTTTGA GGATCCCTGG GTCTTCTGAG ACTGGCCAGG AGAGGGATGG TGGGGCCAGT1500
GCTTGTGTGA AAGCAGGAGG GGCAGCCCTC CTGGACAAGT GTGATCCCCC TATAACGGGC1560
TCTCAGGAGG TTAGTGAGTA GGAGATTCTG CCTTGTTCTG ATGAGCCTGT GCAGGGGCTC1620
CAGGGGAGCA TGCTGTCCAG GGGGCACAGA AGGGTGGTGA GTGTGATCAA ATCTAGTCTC1680
ACTCCCACTT TTTTAGTCTC ACTCCTACTT TTGTCCACCA CCCCTGCCTC CTGGATCTTC1740
TCCCACTTTT TTTTTCAGCT TTAGGACCTG GGGAGATCCT GTGAGTCAAG GCAGACACCC1800
AATCCTGCCC CCACACTCGG GGGTCCTCCC AAGAGGTTGG GGGGCAGAGT CCCAGAGCAG1860
CCCTTTACCC CAGGTCCAGG CCCTGGAATC CTGAGACTCG CGTTTCCTTG GCCAGTGGTA1920
ACACAGGACG TGTGTGCGCA TGTGCAAGTG TGGATGTATG TGTGTGCGTG TGTGTTGCTC1980
ATTTCTTTAG GGAACCTGGG AGTCGGGGTT GGAGGTGCTG GGCAATGGAA CTTCAAATTC2040
AATGTCGCCC AGCAGTGAGG GGAGTCGGGA GGTGAGGCCT GTAGGCCAAC CAATTGGTGG2100
AGTCTCAGCG ATAGCCCAGG TGAGAAGTGG TTCACCCAGA GGGGCAGGGT GGGGGCCTCG2160
GGCAGATCTG TCCCTCTTGG GCACCTCTGT CCTCAAATGT CCAAATGTT GGAGGACCTC2220
TGTTTCATATC CCACGCCTGG GCTCTTGCCA GCAGTGGAGT TACTGTAGAG GGATGTCCCA2280
AGCTTGTTTT CCAATCAGTG TTAAGCTGTT TGAAACTCTC CTGTGTCTGT GTTTTGTGTTG2340
TGCGTGTGTG TGAGAGCACA TCAGTGTGTG CAGGCTGTGT TTCCCCATTT CTCTCCTCCC2400
TTCAGACCCA TCATTGAGAA CAAATGTAAG AAATCCCTTC CCACCACCT CCCTGCCTCC2460
CAGGCCCTCT GCGGGGGAAC CAAGATCACC CAGCATCCTT CCCCACCCCA GCTGTGTATT2520

TATATAGATG GAAATATACT TTATATTTTG TATCATCGTG CCTATAGCCG CTGCCACCGT2580
GTATAAATCC TGGTGTCTGC TCCTTATCCT GGACATGAAT GTATTGTACA CTGACGCGTC2640
CCCACTCCTG TACAGCTGCT TTGTTTCTTT GCAATGCATT GTATGGCTTT ATAAATGATA2700
AAGTTAAAGA AAACCTCAAAA

2720

09646569 "092000

(2) INFORMATION ON SEQ ID NO. 172:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

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CTCAATGCAG AGGATTTAAT CTAAAAGCAT ACAGAAATGC AGCTGAAATT GTGCAGTATG 60
GAGTAAAAAA TAACACCACT TTTCTGGAGT GTGCCCCCAA GTCTCCGCAG GCATCTATCA 120
AGTGGCTGTT ACAGAAAGAC AAAGACAGGA GGAAAGAGGT TAAGCTGAAT GAACGAATAA 180
TAGCCACTTC ACAGGGACTC CTGATCCGCT CTGTTTCAGGG TTCTGACCAA GGACTTTATC 240
ACTGCATTGC TACAGAAAAT AGTTTCAAGC AGACCATAGC CAAGATCAAC TTCAAAGTTT 300
TAGATTCAGA AATGGTGGCT GTTGTGACGG ACAATGGTC CCCGTGGACC TGGGCCAGCT 360
CTGTGAGGGC TTTACCCCTT CACCCGAAGG ACATCATGGG GGCATTTCAGC CACTCAGAAA 420
TGCAGATGAT TAACCAATAC TGCAAAGACA CTCGGCAGCA ACATCAGCAG GGAGATGAAT 480
CACAGAAAAT GAGAGGGGAC TATGGCAAGT TAAAGGCCCT CATCAATAGT CGGAAAAGTA 540
GAAACAGGAG GAATCAGTTG CCAGAGTCAT AATATTTTCT TATGTGGGTC TTATGCTTCC 600
ATTAACAAAT GCTCTGTCTT CAATGATCAA ATTTTGAGCA AAGAACTTG TGCTTTACCA 660
AGGGGAATTA CTGAAAAAGG TGATTACTCC TGAAGTGAGT TTTACACGAA CTGAAATGAG 720
CATGCATTTT CTTGTATGAT AGTGACTAGC ACTAGACATG TCATGGTCCT CATGGTGCAT 780
ATAAATATAT TTAACCTAAC CCAGATTTTA TTTATATCTT TATTCACCTT TTCTTCAAAA 840
TCGATATGGT GGCTGCAAAA CTAGAATTGT TGCATCCCTC AATTGAATGA GGGCCATATC 900
CCTGTGGTAT TCCTTTCCTG CTTTGGGGCT TTAGAATTCT AATTGTCAGT GATTTTGTAT 960
ATGAAAACAA GTTCCAAATC CACAGCTTTT ACGTAGTAAA AGTCATAAAT GCATATGACA1020
GAATGGCTAT CAAAAGAAAT AGAAAAGGAA GACGGCATT TAAAGTTGTAT AAAAACACGA1080
GTTATTCATA AAGAGAAAAT GATGAGTTTT TATGGTTCCA ATGAAATATG TTGGGGTTTT1140
TTTAAGATTG TAAAAATAAT CAGTTACTGG TATCTGTCAC TGACCTTTGT TTCCTTATTC1200

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000260 " 092000

2987

(2) INFORMATION ON SEQ ID NO. 173:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 892 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cdna library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

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TTTTTTCGGG AGGCAGAGTC TCCCTTTGTC GCCAGGCTGG AGTGCAGTGG TGCCATCTCG 60
GCTCACTGCA GCACTGTCTC GGCTCACTGC AGCCTCCGGC CTCCCGTATT CAAGCGATTG 120
TCCTGTCTCA GCCTCCTGAG TAGCTGGGAC TACAGGTGTG CACCACCACG CCCGGCTAAT 180
TTTTGTATTT TTAGTAGAGA CGGGGTTTCA CTGTGTTGGC CAGGATGGTC TCAATCTCGA 240
CCTCGTGATC CNGCCACCT TGGCCTCCCA AAGTGTGGG ATTACAGGCN GTGACTCACC 300
ATGCCAGCC ACTTAGTTTT TTCTTATTCC CACCTTTCTA TCCCATAGAA CACTCTTTT 360
TATCTTCCCT GAACCANTAT TGNATGAGAT AAATANGGGC TGGGGGCTGG GNCCCCGCNT 420
GNGTCACNTC AACANGAGTN ATTTNCCCTT GGNCCGNAGA TNGGAAGTTT TGTNCCCAAT 480
ANGATGNAGC TGCTNGAGTA TCAACAAGGN TGACATTTTT CTGNCTGNCC CNATTTGTGT 540
CCTGGNNNAG ACNGGTNGGT ACCCTGAAGG NCAGANGGCC NAGCTGCCGC AAGACAGCAA 600
NTGACAGTCC ACCTGCCGAC CTGATTCTCTG CATCATGGAA TAANCCACNA TGGCTACCTT 660
CTATCCTCTG TTNCCCAAAT GGTGGNNTGG CACTTATCCT GAAGTCGTCN AATGATTTC 720
CTTTGNAAC TACTTTATTT TACTAATTTA AACTATTTTG TACTGATGTA GCCCTGAGGT 780
ANGTTCATGA AAATGCTGTG CACTCATTCC NATGGAATAA ATGTTGGAAA GCTGATCTTT 840
TCTGATATAA AATGTTGAAT GATANNAAAA AAAAAAAAAA AAAAAAAAAA AA 892

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(2) INFORMATION ON SEQ ID NO. 174:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1679 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cdna library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

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GCACCCACTG GAAACACAGA CGGCACTCTG CGAAAGAGGA AGGGGCGCCA GGAGCTTGGA 60
TTAGAAAAC TGAAGCTTCAA GAACAGACTT GCCTAACAAC AGGAAACTTG TATGTCTCGA 120

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09646569-092000

(2) INFORMATION ON SEQ ID NO. 175:

(A) LENGTH: 2411 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(A) ORGANISM: HUMAN
(C) ORGAN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

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TTCCAACGTT CCCCTTGCGT AAAATGTCCT GGCAAACCAT GGAAGCTTTG ATGCAAGAAC 60
CCTGTTGTAC TGGAGTTTTT CTCCCCTGTG AAAACGTAAC TTAGTGTGG GAGTGAATTG 120
AGGATGTAGA AAGGGTGGTG GAACCAAATT GTGGTCAATG GAAATAGGAG AATATGGTTC 180
TCACTCTTGA GAAAAAACC TAAGATTAGC CCAGGTAGTT GCCTGTAAC TCAGTTTTTC 240
TGCCTGGGTT TGATATAGTT TAGGGTTGGG GTTAGATTAA GATCTAAATT ACATCAGGAC 300
AAAGAGACAG ACTATTAAC CCACAGTTAA TTAAGGACGT ATGTTCCATG TTTATTTGTT 360
AAAGCAGTGT GAATAGCCTT CAAGCATGTG AATAATCTTC CATCTTCCCC GCCACACATA 420
CACACACACA CTTTTTGTTT CTTTCAGGTA GACACCTTTT AAAATGCAGA ACTAACTGAG 480
GCATTTTCAGT AACTTTGCTT TCAAATCAAT AAAGTCAAAT GTATGGAAAC ATTTTGTGCC 540
CTACTCTCCA TACCCCGTGT ACTCAAATTC TCTACTGTAT GAATTATGCT TTAAGTAGAA 600
TTCAGTGCCA AGGAGAACTT GGTGAAATAA ATTATTTTAA TTTTTTTTTT ATCCTTTACA 660
AAGCCATGGA TTTTATTTGG TTGATGTGTG CTCTGTACAC AAGCCATTC AATAGGATGG 720
AGCTGTTAAT TATTTTCCAA AGAGTAATAG ACATGCAAAA GTTTCAATAA AAAGTGGGCC 780
ATTAACAAAT AAATTAATAA ACTAATAAGC ATTCCCTTCT AGGTTTTTCG CAACTGCCT 840
ATCCAATAAC AAATTTGAGA ATCGTTGAAA AAGCTAGTTA TATTCAGAG AAATGATTTT 900
CATTATTGAA ACTGTTCTCC CTAGCAGGCC ATTTTCCCTT TTTCTGGGA GTTTAGCAAG 960
TTTAGGAGAG AATAGTCATG AAAAGAAAGG GAAGAAAGGG GAGAAGGGAA GAGGTTAAAA1020
AGTAAGTGCT CAGACCTATG AACGTAATCC CTTTGCTAGA AATATTTAAG AGCAGCTCAG1080
CTTGGTTGAA ACTGAGTTTT GTCATCTTCC ATATTTGCAG GAAGGTATTT TCTGACTTGC1140
AATGCAGCTA GATGTAAAAT TTTATTTTAT CATACTAGAA AGCCTTGACT AGAAAAATGA1200
ATAAATATTG AGGGTTTCCT GTCCATATCT GGCTTGCATG TGCCAGAAAG CAGAGAATAG1260
AAAATGTAAT CTCCAACATC CAAGCATCGA AACCCAAGGG GTAGGCAATT CTATGTAGGT1320
TTTGGACATG AAGTTTGGTG CATCTTGGTT TATGCTGGCT CAACTGCTAT TAAACCTCTC1380
TGGCTTATAG TCTCTTCATT CTATTAGACA AGCACGTATC GAACACTTGC TTCGCACAAG1440
GCTCTTTAGT TAACAATTTA GCAGCTACTG TTTGTGTAA ACACACTTTT CACCAAATAG1500
GTTCTGAGGC AAACGAGAGC AATGACTATT TAAAGAAAGG CTTTCCCAGC ATCACTTACA1560
CATCCCAAAA CTAAAAAGAT CAACTCTTCC AACTGAGAAA AGACTCCTGG CTTTGAATGG1620
AACTTACAG CAGAGAGTCA CAGGCCACGG CAACAACAAC GACAACAACA AACATTTGGA1680
ATATTATTCT CAACTCACGT TTTAATAATA CATCTTATTA TTTTCTAGT AGAGAACTA1740
CAAATCAGCC TCTTCAACAT TTATATACAG TTTAATAAGC CTCTTGCAAG TTAGTGTTC1800
TCTCACCTGA GGTATTTTTT TCCTCCCCAC CTTGCCCCTG TCCTCCCTT CCTCTCTCC1860
CTTTGCAAGA GGAAATATTT AACATATTTG GGTCCAACCT CAATAATGTA ATAATTAATA1920
CATTAAAAGC ATTTAAGTTC CTTTCTAGAA AAATGCACAG GCTAAGGCAT AGACAAAACA1980
AAGAGAAATG CTGAGAAATT TGCCACTGGA GACAAGCAAT CTGAATAAAT ATTTGCCAAA2040
AGTTCTTTTT ATGTCATATA GTGTCAGGAT TTGAAGGAGC TATTTTTTTT TAATGTTGCA2100
ACTAGCAACT CATCTTCGGA AGACACAGCC AGGAGAATGA AGTAGAAGTG AAAGGTTTAT2160
AAATCCATTT GTAAGCATTT ATCCCATATA TTTTAAATTC AAGAAAAATT GTGTTTATCT2220
TTAGAATTTT GTATTCAATA CTTTATGTAC TATGTGACTC ATGCTTCTGG ATAAATAAAG2280
CACCAAATAT GTATCTGTAA CCACAATCAC ACATATTATA TTAAATATAT ATCTATATAA2340
CAGCCAAAAA AAAAAAAAAA AAACACAAGA AAAAGAAAGG GAGAGGGGGG GGGAGAGAAG2400
GGGGGGGAGG T

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2411

00250"6954960

(2) INFORMATION ON SEQ ID NO. 176:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3450 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: partial cDNAs produced from individual
ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

000260" 69594960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

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CTCGTCCCAA ACCAGGACAC CCTCTCTACA GTAAATACAT GCGTGGGGAT GTACTTGTGA 60
TGCTGAAGCA GACGGAAAAT AATTACTTGG AGTGCCAAAA GGGAGAAGAC ACTGGCAGAG 120
TTCACCTGTG TCAAATGAAG ATTATCACTC CACTTGATGA ACATCTTAGA AGCAGACCAA 180
ACGATCCAA( CCACGCTCAG AAGCCTGTTG ACAGTGGTGC TCCTCATGCT GTCGTTCTTC 240
ATGATTTTCC AGCAGAGCAA GTTGATGATT TGAACCTCAC TTCTGGAGAA ATTGGTTTAT 300
CTTCTGGAG AGATAGATAC AGATTGGTAC AGAGGGAAC GTAGAAACCA GATTGGCATA 360
TTTCCTGCC ACTATGTCAA AGTGATTATT GATATCCCAG AAGGAGGAAA TGGGAAAAGA 420
GAATGTGTT CATCTCATTG TGTAAAGGC TCAAGATGTG TTGCTCGGTT TGAATATATT 480
GGAGAGCAC AGGATGAGTT GAGTTTCTCA GAGGGAGAAA TTATTATTCT TAAAGAGTAT 540
GTGAATGAG AATGGGCCAG AGGAGAAGTT CGAGGCAGAA CTGGGATTTT CCCCTGAAC 600
TTTGTGGAG CTGTTGAGGA TTATCCCACC TCTGGTGCAA ATGTTTTAAG CACAAAGGTA 660
CCACTGAA( CCAAAAAAGA AGATTCTGGC TCAAACCTCT AGGTTAACAG TCTTCCGGCA 720
GAATGGTG( AAGCTCTTCA CAGTTTTACA GCAGAGACCA GTGATGACTT ATCATTCAAG 780
AGGGGAGAG( GGATCCAGAT TCTGGAACGT CTGGATTCTG ACTGGTGCAG GGGCAGACTG 840
CAGGACAG( AGGGGATCTT CCCAGCAGTG TTTGTGAGGC CCTGCCCAGC TGAGGCAAAA 900
AGTATGTT( CCATAGTACC GAAGGGGCAG GAAGGCCAAA GCCTTATATG ATTTCCGAGG 960
GGAGAATGA GATGAACTTT CCTTCAAGGC TGGAGATATA ATAACAGAGC TGGAATCTGT1020
AGATGATG( TGGATGAGTG GAGAACTTAT GGGAAAATCT GGAATATTTT CCAAAAACTA1080
CATACAGT( CTACAGATCA GCTAGAGGAG AAGCTTGTCT GTGTTCCCTT GCACAAGAAC1140
TCACTTGA( TATCACCTTG ACTATCAGAT ATGTTTTTGC ACTATTTTTT TTAAGTAAA1200
AAGAAATAC TAAGCTGTAC ATGGTACACT AGAATTTTCT GAAAGCAGAA AACGTTCA1260
TTTTGTAGT AATTTTCATT ACAATAGAAA CATGCACATG GAAACCCATG AGCTAGGATT1320
CTACCGAGA AAACATCTAG TGGGATTAGC AAGGTGAAGG GAAAGCATCT GGTGGCATGG1380
CAGCATGGG AGGCTCACAC ACAGAAGTTG CACGTGGACA TCTGTTTAA TCAGCACAAG1440
TGAATTAA( ATGCTTCTTC ATTTTTTTTAC TTTAGTTAAA AAAGAGGACA TTTAATATTC1500
TACATGCT( AACTATCAGG ACATGGTTAG CAATCTCAAT TTCATTTTGT ATATTCAAAT1560
TAATTCTT( AGCTTGAGCA TATCAGCCTT ATTACCAGAG CAAATCCTTC CTTCAGATGG1620
GATAGTTT( TGAAGATTG GAGCATTTGT AAGCACATGG TGAAATCAGC CCCTGCCCAC1680
CAAAATAA( TTTATGTTAC CAAGTGATTC CCATTTGTCT AAGGATTTGA AGGGGGTCTA1740
AATTGGAT( ATCTTAGTCT AAAGAACCAA AACCATCCCT GAAATGCCTT GCTAATACAA1800
CTAATCCT( CATATATGTG CCATACTTAT TTTTTTCTC AGTGTATACT TTATGTTAAC1860
AGGGTTATTA CAAAGCACAT TTTCTGAATC TGCAATCATT CCTTTGACAA TTAAGTGGAC1920
CAAAGGAAAA TTCATTTTCT TTGCATTATT CCAGTAATAT ATAAAAACTG TGTCTTGTTA1980
TAGTAGTACA TTATGAATCA CATATAAAAT CTTACAATAC AGAACAAC TG TTAAGATGGA2040

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002260" 59594960

AAACAGTGCC AAACCTCCAC AGCTCATTTT TTTGTAATAT AATCAGAATG AAAAATAATT2100
 TAAGAGGACA GAAGACTGGT ACTTTTTTGT TTTATTTTTT CTCTAGCTTA TCCCTGCACA2160
 ATTATTAGAG TGAATGAAAA ACCACTTTCC TGCTTTCCAT TGTATAAAT TCTAAGCTTA2220
 AGATAAAAGT GGTTCCTTAC ATGACTGAAT CAATTACAAT TTATGGGCTA GAGCCAAATA2280
 GGTGAAGAC AATCATCCAA ACAGATCAAT GGAATAGAAT TTCATTGGAA ATGTAAAACA2340
 CTTTCCCAAC AATGGTCATG ACTTTCTTCT GTTTTGGAGA AGAGTTTCAT ATGCTGGACC2400
 ACATTTTAGC TTTTATTGTT TTTTTTTTCC CATTGTCCAA AAAGTTAAGC AACAAAGTGGC2460
 CACACTTTTA CGTGACTIONA ACCTGGAGTT CTGCAAAGAA GGTAATATTT ACTTGGTCTT2520
 TGACTIONAAGT TATCTCCCCA TTCTATGGTT ACATTTTATT TTGGACTATG GGGACTTCTA2580
 ATACGTTTTG GTAAAGAAGA GAGTATAAAG AAAATTCTTG TCAAATTTCA CTCAAAAGTA2640
 ATTTTCATGAG AAATCAATGA TTTAAAGCAT TATCCAAATT AAATTATCAT TTGCAGCAAA2700
 CTGTACAACA GCAGGAAGGA TATGGAATGG AACATGAGGT ATATATCTTT GCCTTTATAA2760
 TTTTAACATC TTATATTGAA GATTCTGAAA ACCTATCTTT ATTAGAGGAA AATCTCAATC2820
 TTCAGTTTTG GCCTTCTGTC ACCAGAATGA TAAGTGCAAT AGTTGTAAAT CTACTTGACA2880
 CTGTAATAAA CTGAACTGAA CTTTCAAAAT CCCTTTCTCA TACTAGACTG AGTTTTTTGA2940
 GAATGGAGGT GGAACCTTTT TTTTTTTTTT TTGTGAGACA GGATTAAATT CCCTTCGACC3000
 CAGGCTGGAG TGCAATGCAA TGTTGGCTCA CTGCAGCCTC TGCCTCCTGG GGCTCAAAGT3060
 GATTCTCCTG CCACAGCCTC CTGAGTAGCT GGGACTACAG GCGCACACCA CCCGTGCCCA3120
 GCTAATTTCT GGTATTTTTT TTTCTTTTGT TAGAGACAGG GTTTCGCCAT GTTGCCAGG3180
 CTGGGTTTCA AACACCTGGG CTCAAGCAGT CTGCCTGCCT CAGCCTCCCA AAGTGCTGGT3240
 AATACTGCAC CTGGGCCTGT GGTACCTTAT TTATCTTTGT ATCTCTAGTC CTTTGCACCA3300
 TTCAGCCTCA ATAAAGGTTG GTTGGTGGGT TGGGTGAGTT GGTGGTTGG AATGGATGGA3360
 TGGATGGATG AATGACTTTC ACATACAGCA ATACCATCTT GGATTCACCT AATATCTTTC3420
 CTCTTTAATT TTTGACATAA ATCTATACTA 3450

(2) INFORMATION ON SEQ ID NO. 177:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 874 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CGGGGGCGAG	CCGGGCCCTGC	GCGGTAGTGG	GACCCGACCC	TGCTCCAGT	GGGCGTCTTG	60
GGCCCCGGCT	CTATTCTGGG	CTGCGGCCCT	GGGAAGGGCT	CGCCGGGTGC	CAAATGAGCT	120
GTCTTAAGCT	TCGCGGGGCTG	CAGCTTCCTG	CATGATGCTG	GGGAGCTTGG	CGCCTGACCC	180
AGGATCTAGA	AGGCACTCTG	GGCAGGCCGC	GCTCCGCCCA	CGAAGGTACC	CAACCTCTG	240
GGATAGATGC	AGGAAGCGAT	GGTTAAGACC	CATTTTCACC	CAACTTCTCG	CCGCAGTCTG	300
GCTTACCACA	CGCTCCTCCC	CATTCCCAGT	GAGCCGCTTT	TTGCAGCACC	AGGCGAACAC	360
TTACACCAGT	GCTTTGTAAA	GGAATCTTAT	TGTCCACCCC	GTGTCTTGGC	AAAAGAACAG	420
TGATCACACA	GATTCTACT	TGGGCTCTTT	CCTTTAATCT	TCGGAGGCTG	AGTTTGCCCA	480
ACTCAGGTTT	AACCACCAAG	GA CTCTGAGA	GCTGGCAGGT	CTGAGTAACC	CTGGTAACAA	540
TTCTCTTCAC	CTTATCAAAA	CCTGAGCTAA	AACCAATGCA	TCAGCTGATG	ATGACAGCAG	600
AGAGTGGCAG	GGCTGAGGAC	CCAAAGTCAT	TTCCCAGGCT	GGCGGAGAAT	AAACTGCCAG	660
GGAGAAGAAT	GAGAAGACAG	GAGACAACT	GTTTGGAAG	CTAAATCTTC	CCTCTTAATG	720
AATAAAGGTT	TTTGCCTTGT	CTTAAAAAAT	AACAGGAAGA	AGCAGGGAAA	AATAAATAAC	780
TTATGGTAAT	CTGGAATTGT	ATTTTGTAAAT	ATTAAGTGTT	TTGAACCTCT	AACATTTACC	840
TTCCCCAAAA	ATCGAACCTT	CAGGTTTCAA	AAAT			874

(2) INFORMATION ON SEQ ID NO. 178:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3265 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

TACTTCTGCA	TGATGACAGA	AGCCGAGCAG	GACAAAGTGGC	AGGCTGTGCT	GCAGGACTGC	60
ATCCGGCACT	GCAACAATGG	AATCCCTGAG	GACTCCAAGG	TAGAGGGCCC	TGCGTTTACA	120
GATGCCATCC	GCATGTACCG	ACAGTCCAAG	GAGCTGTACG	GCACCTGGGA	GATGCTGTGT	180
GGGAACGAGG	TGCAGATCCT	GAGCAACCTG	GTGATGGAGG	AGCTGGGCCC	TGAGCTGAAG	240
GCAGAGCTCG	GCCCCGCGGCT	GAAGGGGAAA	CCGCAGGAGC	GGCAGCGGCA	GTGGATCCAG	300
ATCTCGGACG	CCGTGTACCA	CATGGTGTAC	GAGCAGGCCA	AGGCGCGCTT	CGAGGAGGTG	360
CTGTCCAAGG	TGCAGCAGGT	GCAGCCGGCC	ATGCAGGCCG	TCATCCGAAC	TGACATGGAC	420
CAAATTATCA	CCTCCAAGGA	GCACCTTGCC	AGCAAGATCC	GAGCCTTCAT	CCTCCCCAAG	480
GCAGAGGTGT	GCGTGC GGAA	CCATGTCCAG	CCCTACATCC	CATCCATCCT	GGAGGGCCCTG	540

3265

(2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 262 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

SLCVFPSSAA SFLSFLALVV AATMNKKKKP FLGMPAPLGY VPGLGRGATG FTTRSDIGPA 60
 RDANDPVDDR HAPPGKRTVG DQMKKNQAAD DDEDLNDTN YDEFNGYAGS LFSSGPYEKD 120
 DEEADAIYAA LDKRMDERRK ERREQREKEE IEKYRMERPK IQQQFSDLKR KLAEVTEEEW 180
 LSIPEVG DAR NKRQRNPRYE KLTPVPDSFF AKHLOTGENH TSVDPRTQF GGLNTPYPGG 240
 LNTYPYGGMT PGLMTPGTVS WT 262

(2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 467 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

HTLSRWTKHS IPRWNDARTD DTWHSELDNR KIGQARNTLM DMRLSQVSDS VSGQTVVDPK 60
 GYLTDLNSMI PTHGGDINDI KKRLLLLKSV RETNPHHPPA WIASARLEEV TGKLQVARNL 120
 IMKGTEMCPK SEDVWLEAAR LQPGDTAKV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR 180
 VLRKALEHVP NSVRLWKAAR ELEEPEDARI MLSSRAVECCP TSVELWLALA RLETYENARK 240
 VLNKARENIP TDRHIWITAA KLEEANGNTQ MVEKIIDRAI TSLRANGVEI NREQWIQDAE 300
 ECDRAGSVAT CQAVMRAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP 360
 SKKSVWLRAA YFEKNHGTRE SLEALLQRAV AHCPKAEVLW LMGAKSKWLA GDVPAARSIL 420
 ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLAKARTV PPPPGCS 467

(2) INFORMATION ON SEQ ID NO. 181:

(A) LENGTH: 284 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

VRAGPEAAGQ	GADSAPTARV	FMKSVKLEWV	QDNIRAAQDL	CEEALRHYED	FPKLWMMKGQ	60
IEEQKEMMEK	AREAYNQGLK	KCPHSTPLWL	LLSRLEEKIG	QLTRARAILE	KSRLKNPKNP	120
GLWLESVRLE	YRAGLKNIAN	TLMAKALQEC	PNSGIDLWSEA	IFLEARPQRR	TKSVDALKKC	180
EHDPHVLLAV	AKLFSWQRKI	TKAREWFHRT	VKIDSDLGDA	WAFFYKFELQ	HGTEEQQEEV	240
RKRCESAEPR	HGELWCAVSK	DIANWQKKIG	DILRLVAGRI	KNTF		284

(2) INFORMATION ON SEQ ID NO. 182:

(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

QPGIKESILM KETQGPYQGQ FLGQDSHQHI THVLLGREKQ YIPVERSQSI SGRNVVKGGR 60
CYAAAPSVPE VAVIP 75

(2) INFORMATION ON SEQ ID NO. 183:

(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

TFLLSLSYSS SRYFSQEFQR RLLKCLLAA QYQSINYPFW GLALEIIFVG RPNSSQQGSQ 60
ACLLDLFPLR GRNEL 75

(2) INFORMATION ON SEQ ID NO. 184:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 117 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

QGTRHPQSLS HKPAKKIDVA RVTFDLYKLN PQDFIGCLNV KATFYDTYSL SYDLHCCGAK 60
RIMKEAFRWA LFSMQATGHV LLGTSCYLQQ LLDATEEGQP PKGKASSLIP TCLKILQ 117

(2) INFORMATION ON SEQ ID NO. 185:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 143 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

KSAAQTAMTT PPQTPPHYPF INRQDFPCIL LRISSSHSPA PSPMSWLHHC KTDLLQGSQK 60
LLLALYHFYP HLPPEATATIH SHCPSALRPS SRADGSMVIL SWVVLLKPSQ GADSQRASRV 120
SGLDDSKEGT PIFIKTDIP RGF 143

000269-092000

(2) INFORMATION ON SEQ ID NO. 186:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

TQTRHFQLAT QSGRAGGNTD LDIHKKIKPK IKHSILCPLK GLIKGTQSPP RSPLPCQHHK 60
ASSAHTKGLG RGILLPPHQP QEWT 84

(2) INFORMATION ON SEQ ID NO. 187:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

RHWGFTASIF SLKRFITSTS KEQTNWRNVC FFFLFIKFYS TAKFQISFTY RPCKGTVRTE 60
HLFYLRDQGV EIFSLNFIRK GWVQWLMPVI SAFWEAEAGR SLVARSLRPA WATQ 114

(2) INFORMATION ON SEQ ID NO. 188:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```

NLINKKKKKHT  FLQLVCSLLV  EVINRFKEKI  LAVNPOCLQL  FWQNIFKEIQ  QANFEVLMKV  60
KEGGISSFGR   NEKCLTRDIT  THVSGSCFLP  KTFREEVN   98

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

KYELYTENAT	TEKTEPNSQE	DKNDGGKSRK	GNIELASSEP	QHFTTTVTRC	SPTVAFVEFP	60
SSPQLKNDVS	EEKDQKKPEN	EMSGKVELVL	SQKVVKPKSP	EPEATLTFFP	LDKMPEANQL	120
HLPNLNSQVD	SPSSEKSPVM	TPFKFWAWDP	EEERRRQEKW	QQEQERLLQE	RYQKEQDKLK	180
EEWEKAQKEV	EEEERRYYEE	ERKIIEDTVV	PFTVSSSSAD	QLSTSSSMTE	SGGTMNKIDL	240
GNCQDEKQDR	RWKKSFOGDD	SDLLLKTRES	DRLEEKGSLT	EGALAHSGNP	VSKGVHEDHQ	300
LDTEAGAPHC	GTNPQLAQDP	SQNQOTSNTPT	HSSDEVKPKT	LPLDKSINHQ	IESPSERRKS	360
ISGKKLCSSC	GLPLGKGAAM	IIETLNLNLYFH	IQCFRCGICK	GQLGDAVSGT	DVRIRNGLLN	420
CNDCYMRSRs	AGOPTTL					437

(ii) MOLECULE TYPE: ORF

(A) ORGANISM: HUMAN

SANHKLEVNG	TDGLAPVEVE	ELLRQASERN	SKSPTEYHEP	VYANPFYRPT	TPQRETVTGP	60
PNFQERIKIK	TNGLGIGVNE	SIHNMGNGLS	EERGNNFNHI	SPIPPVPHPR	SVIQQAAEKL	120
HTPQKRLMTP	WEESNVMQDK	DAPSPKPRLS	PRETIFGKSE	HQNSSPTCOE	DEEDVRYNIV	180
HSLPPDINDT	EPVTMIFMGY	QQAEDSEEDK	KFLTGYDGII	HAELVVIDDE	EEEDEGEAEK	240
PSYHPIAPHS	QVYQPAKPTP	LPRKRSEASP	HENTNHKSPH	KNSISLKEQE	ESLGSPVHHS	300
PFAOTTTGDG	TEDPSLTALR	MRMAKLGGKV	I			33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
RGAGTQPGPL LKKPYQPRIK ISKTSVDGDP HFVVDFFPLSR LTVCFNIDGQ PGDILRLVSD 60
HRDSGVTVNG ELIGAPAPPN GHKKQRTYLR TITILINKPE RSYLEITPSR VILDGGDRLV 120
LPCNQSVVVG SWGLEVSVSA NANVTVTIQG SIAFVILIHL YKKPAPFQRH HLGFIYANSE 180
GLSSNCHGLL GQFLNQDARL TEDPAGPSQN LTHPLLLQVG EGPEAVLTVK GHQVPVVWKQ 240

RKIYNGEEQI DCWFARNNA KIDGEYKDY LASHPFDTGM TLGQGMSREL 290
```

(2) INFORMATION ON SEQ ID NO. 193:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 87 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```
GHGSYRTPKR SSTNCLGKFW ELADAKKKRK KVHQKQKRAT IRATELAKGK RHVGGSVSHL 60
SPGTVKCVIT AQVHGKRQQQ KALCRLE 87
```

(2) INFORMATION ON SEQ ID NO. 194:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 82 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

```
QFIQGMCSRK FAWYLFVKHL KVPQIGFKVP GAVGWHDPR KATEHPARLL HRAGEVTFYL 60
FFRLHPIFHL PFLQRAQGAI IF 82
```

000260"69594960

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 251 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

```

DDRSFHFHHH KSVIDAMKGR PGQSPLFRPS QGTGRVPGTR QMLQDSVQAA LEEVAASEAL 60
LGPLSPPGKS RDGNASAGEG CQVFRSPPSE VSPPPGQDTP TSTFLKRRWD SQVTLLPSKK 120
CKSQQLQESV SQFPSPGGR REGPWSSLGA GGPSSHISAK YFPLPVQPAC PCTSLEAGHR 180
PGRCVDLQES QGVDHPANLR LSSGTSCRRG LNPTPVQVRS HEASSQVKMH QTVTWRFYTF 240
LNFAQLGACL L 251

```

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 149 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```

FAKGLDRERG NMNLDREGDT IERRTLPTLQ ASDLPFEGTL DGGRGRGLGL SYSHELLAST 60
DSSNSPPHKI TGTNIFNFAY LFLGEFPPSL FCPETTCKAL HFEREEKLFG TTPMIFFFVI 120
LEIYFFIILI ADVLFIYLIC IRSNNRKL 149

```

(2) INFORMATION ON SEQ ID NO. 197:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein

000260" 69594960

```
(ii) MOLECULE TYPE: ORF
(iii) HYPOTHETICAL: yes
(vi) ORIGIN
      (A) ORGANISM: HUMAN
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:
```

(2) INFORMATION ON SEQ ID NO. 198:

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

(2) INFORMATION ON SEQ ID NO. 199:

(vi) ORIGIN
(A) ORGANISM: HUMAN

QCRGFNLKAY	RNAAEIVQYG	VKNNTTFLC	APKSPQASIK	WLLQKDKDRR	KEVKLNERII	60
ATSQGLLIRS	VQSDQGLYH	CIATENSFKQ	TIKINFKVL	DSEMVAVVTD	KWSPWTWASS	120
VRALPFHPKD	IMGAFSHSEM	QMINQYCKDT	RQHQOGDES	QKMRGDYGKL	KALINSRKS	180
NRNQLPES						189

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 97 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```
FFREAESPFV ARLECSGAIS AHCSTVSAHC SLRPPVFKRF SCLSLSSWD YRCAPPRPAN 60
FCIFSRDGVLS LCWPGWSOSR PRDPAHLGLP KCWDYRX 97
```

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 250 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

(2) INFORMATION ON SEO ID NO. 202:

- EKTPGFEWKL TAESHRPRQQ QRQQOTFGIL FSTHVLIIHL IIFLVEKLQI SLFNIYIQFN 60
KPLASYLFSL LRYFFPPHLA PVPPFLFSLC KRKYLTYLGP TSIM 104

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 93 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- ```

HKKNFWQIFI QIACLQWQIS QHFSLFCLCL SLCIFLERKL NAFNVLIITL LKLDPNMLNI 60
SSCKGRRGRE EOGQGEEKN TSGERTSNLO EAY 93

```

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RPKPGHPLYL KYMRGDVLVM LKQTENNYLE CQKGEDTGRV HLSQMKIITP LDEHLRSRPN 60  
 DPSHAQKPVD SGAPHAVVLH DFPAEQVDDL NLTSGEIGLS SGEDRYRLVQ REL 113

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 225 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

TSLLEKLVYL LEKIDTDWYR GNCRNQIGIF PANYVKVIID IPEGGNGKRE CVSSHCVKGS 60  
 RCVARFEYIG EQKDELSFSE GEIIILKEYV NEEWARGEVR GRTGIFPLNF VEPVEDYPTS 120  
 GANVLSTKVP LKTKKEDSGS NSQVNSLP AE WCEALHSFTA ETSDDLSEFKR GDRIQILERL 180  
 DSDWCRGRLQ DREGIFPAVF VRPCPAEAKS MLAIVPKGQE GQSLI 225

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 105 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear

000250" 69594960

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

CIGFSSGFDK VKRIVTRVTQ TCQLSESLVV KPELGKLSLR RLKERAQVGI CVITVLLPRH 60  
 GVDNKIPLQS TGVSVRLVLQ KAAHWEWGGA CGKPDCEKL GENGS 105

(2) INFORMATION ON SEQ ID NO. 207:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 83 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

LCGAAASCMM LGSLAPDPGS RRHSGQAALR PRRYPTLWDR CRKRWLRPIF TQLLAHVWLT 60  
 TRSSFPFVSR FLQHQAQNTYT SAL 83

(2) INFORMATION ON SEQ ID NO. 208:

- (i) SEQUENCE CHARACTERISTIC:
  - (A) LENGTH: 581 amino acids
  - (B) TYPE: Protein
  - (C) STRAND: individual
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
  - (A) ORGANISM: HUMAN

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|             |            |             |            |             |            |     |
|-------------|------------|-------------|------------|-------------|------------|-----|
| YFCMMTEAEQ  | DKWQAVLQDC | IRHCNNGIPE  | DSKVEGPAFT | DAIRMYRQSK  | ELYGTWEMLC | 60  |
| GNEVQILSNL  | VMEELGPELK | AELGPRLKKG  | PQERQRQWIQ | ISDAVYHVMV  | EQAKARFEEV | 120 |
| LSKVQQVQPA  | MQAVIRTDMD | QIITSKEHLA  | SKIRAFILPK | AEVCVRNHVQ  | PYIPSILEAL | 180 |
| MVPTSQGFTE  | VRDVFFKEVT | DMNLNVINEG  | GIDKLGEYME | KLSRLAYHPL  | KMQSCYЕКME | 240 |
| SLRLDGLQQR  | FDVSSTSVFK | QRAQIHMREQ  | MDNAVYTFET | LLHQELGKGP  | TKEELCKSIQ | 300 |
| RVLERVLKIKY | DYDSSSVRKR | FFREALLOIS  | IPFLLKKLAP | TCKSELPRFQ  | ELIFEDFARF | 360 |
| ILVENTYEEV  | VLQTVMKDIL | QAVKEAAVQR  | KHNLYRDSMV | MHNSDPNLHL  | LAEGAPIDWG | 420 |
| EEYSNSGGGG  | SPAPAPRSQP | PSRKS DGAPS | RWSLWSRMRR | WGCPRLRLALS | HHHLRPRTVS | 480 |
| LRSEACWPKV  | CGLRAPHQPA | PCSTGPPLGR  | VPSLRPPPRP | PRRLPHPSI   | SCLERLWTLG | 540 |
| PPSPATRRL   | SRCPAPAATP | PSTPPPRTVQ  | GCLRSSRPVG | P           |            | 581 |

(i) SEQUENCE CHARACTERISTIC:  
(A) LENGTH: 466 amino acids  
(B) TYPE: Protein  
(C) STRAND: individual  
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: yes

(vi) ORIGIN  
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

|            |            |            |            |             |            |     |
|------------|------------|------------|------------|-------------|------------|-----|
| PQRAAPPPHP | GPQRPPAWRA | VAFPRGWLTP | GCWGWAAAPA | AVAVLLAPVD  | GGALGQQVQV | 60  |
| GVAVVHDHAV | PVEVVLPLHR | GLLHSLQDVL | HDGLQHLLLV | RVFHQDEPGK  | VLEDQLLEPG | 120 |
| QLRLAGRGQL | LEQERDADLQ | QRLPEEPLPH | RAAVVVVFLQ | HPLQDPLDGL  | AQLLLGGPLP | 180 |
| QLLVQEGLER | IHGIVHLLPH | VDLGSLLHGG | RAGHIKSLAQ | PVQSQRLLHL  | IAALHLQGVV | 240 |
| RQPQQLLHVL | AQLVNAALVD | DVQVHVRDLL | EEDISHLSEA | LAGGDHQGLQ  | DGWDVGLDMV | 300 |
| PHAHLCLGED | EGSDLAGKVL | LGGDNLVHVS | SDDGLHGRLH | LLHLGQHLLLE | ARLGLLVHHV | 360 |
| VHGVRDLPL  | PLPLRFLQ   | PRAELCLQLR | AQLLHHQVAQ | DLHLVPTQHL  | PGAVQLLGLS | 420 |
| VHADGICERR | ALYLGVLGRS | IVAVPDAVLQ | HSLPLVLLGF | CHHAEV      |            | 466 |

WO 99/47655

PCT/DE99/00909

**Claims**

1. A nucleic acid sequence that codes a gene product or a part thereof, comprising

a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-5, 10-12, 14, 15, 19, 21-25, 28, 30, 31, 34, 37, 43, 45, 48, 50, 51, 58-65, 68, 69, 71, 72, 74, 76 and 161-178, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, characterized in that it is expressed elevated in normal breast tissue.

4. BAC, PAC and Cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID No. 1 to Seq. ID No. 76 and Seq. ID No. 161 to Seq. ID No. 178, for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

0002650" 69594960

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

9. A nucleic acid sequence according to claims 1 to 7,  
wherein the size of the fragment has a length of at least 150 to  
4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.





32. A nucleic acid sequence according to claims 1 to 10,  
wherein it is an mRNA sequence.

34. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

36. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 300 to 3500 bp.

37. The nucleic acid sequences Seq. ID No.: 3, 37, 45, wherein they are associated with lipometabolism and can be used for treatment of pathological alterations of the lipometabolism.

## DECLARATION FOR PATENT APPLICATION

51572

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original first and sole inventor (if only one name is listed below) or an original first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

## HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE

the specification of which

is attached hereto

was filed on 19 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00909 and (if applicable) was amended on

I hereby authorize our attorneys to insert the serial number assigned to this application

I hereby state that I have reviewed and understand the contents of the above-identified specification including the claims as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56

I hereby claim foreign priority benefits under 35 U.S.C. §119(a)-(d) or §365(b) of any foreign application(s) for patent or inventor's certificate, or §365(a) of any PCT International application which designated at least one country other than the United States listed below and have also identified below, by checking the box any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed

## PRIOR FOREIGN/PCT APPLICATION(S) AND ANY PRIORITY CLAIMS UNDER 35 USC §119

| APPLICATION NO. | COUNTRY | DAY/MONTH/YEAR FILED | PRIORITY CLAIMED |
|-----------------|---------|----------------------|------------------|
| 198 13 835.0    | GERMANY | 20/03/98             | YES              |

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below

## PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)

| APPLICATION NUMBER | FILING DATE |
|--------------------|-------------|
|                    |             |

I hereby claim the benefit under 35 U.S.C. §120 of any United States application, or §365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. §112

I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

## PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120

| APPLICATION NO. | FILING DATE | STATUS — PATENTED, PENDING, ABANDONED |
|-----------------|-------------|---------------------------------------|
|                 |             |                                       |

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected herewith: William Millen (19,544); John L. White (17,746); Anthony J. Zelano (27,969); Alan E. J. Branigan (20,565); John R. Moses (24,983); Harry B. Shubin (32,004); Brian P. Heaney (32,542); Richard J. Traverso (30,595); John A. Sopp (33,103); Richard M. Lebovitz (37,067); John H. Thomas (33,460); Catherine M. Joyce (40,668); Nancy J. Axelrod (44,014); James T. Moore (35,619); James E. Ruland (40,921) and Jennifer J. Branigan (37,432)

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2200 Clarendon Boulevard

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16

## Declaration for Patent Application (Continued)

51572

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

|      |                                                                            |                               |
|------|----------------------------------------------------------------------------|-------------------------------|
| -00  | Full Name of sole or first inventor (given name family name)               |                               |
|      | Thomas SPECHT                                                              |                               |
|      | Signature <i>Thomas Specht</i>                                             | Date <i>16.08.00</i>          |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany              |                               |
| 2-00 | Full Name of additional joint inventor (given name family name)            |                               |
|      | Bernd HINZMANN                                                             |                               |
|      | Signature <i>Bernd Hinzmann</i>                                            | Date <i>17.08.00</i>          |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Parkstrasse 19, D-13127 Berlin, Germany                |                               |
| 3-00 | Full Name of additional joint inventor (given name family name)            |                               |
|      | Armin SCHMITT                                                              |                               |
|      | Signature <i>Armin Schmitt</i>                                             | Date <i>September 4, 2000</i> |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Laubacher Strasse 6/II, D-14197 Berlin, Germany        |                               |
| 4-00 | Full Name of additional joint inventor (given name family name)            |                               |
|      | Christian PILARSKY                                                         |                               |
|      | Signature <i>Christian Pilarsky</i>                                        | Date <i>10.08.00</i>          |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany |                               |
| 5-00 | Full Name of additional joint inventor (given name family name)            |                               |
|      | Edgar DAHL                                                                 |                               |
|      | Signature <i>Edgar Dahl</i>                                                | Date <i>10.08.2000</i>        |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Eleonore-Prochaska-Strasse 6, D-14480 Potsdam, Germany |                               |
| 6-00 | Full Name of additional joint inventor (given name family name)            |                               |
|      | André ROSENTHAL                                                            |                               |
|      | Signature <i>André Rosenthal</i>                                           | Date <i>29/8/00</i>           |
|      | Residence <i>DEX</i>                                                       | Citizenship German            |
|      | Post Office Address Koppenplatz 10, D-10115 Berlin, Germany                |                               |

□ Additional joint inventors are named on separately numbered sheets attached hereto

## DECLARATION FOR PATENT APPLICATION

51572

As a below named inventor, I hereby declare that

My residence, post office address and citizenship are as stated below next to my name.

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**HUMAN NUCLEIC ACID SEQUENCES FROM NORMAL BREAST TISSUE**

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☐ is attached hereto

☒ was filed on 19 MARCH 1999 as United States Application Number or PCT International Application Number PCT/DE99/00909 and (if applicable) was amended on \_\_\_\_\_

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**PROVISIONAL APPLICATION(S) UNDER 35 U.S.C. §119(e)**

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I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application

**PRIOR U.S./PCT INTERNATIONAL APPLICATION(S) DESIGNATED FOR BENEFIT UNDER 37 U.S.C. §120**

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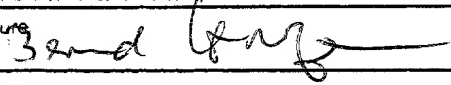

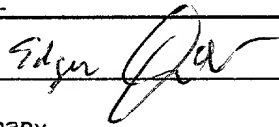
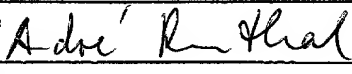
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2200 Clarendon Boulevard  
Arlington, VA 22201  
TEL (703) 243-6333  
FAX (703) 243-6410

Declaration for Patent Application (Continued)

515-2

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

|                                                                                                    |                       |
|----------------------------------------------------------------------------------------------------|-----------------------|
| Full Name of sole or first inventor (given name family name)                                       |                       |
| Thomas SPECHT                                                                                      |                       |
| Signature<br>X    | Date<br>X 10.08.00    |
| Residence<br>Berlin Germany                                                                        | Citizenship<br>German |
| Post Office Address Grabenstrasse 14, D-12209 Berlin, Germany                                      |                       |
| Full Name of additional joint inventor (given name family name)                                    |                       |
| Bernd HINZMANN                                                                                     |                       |
| Signature<br>X    | Date<br>X 17.08.00    |
| Residence<br>Berlin Germany                                                                        | Citizenship<br>German |
| Post Office Address Parkstrasse 19 D-13127 Berlin, Germany                                         |                       |
| Full Name of additional joint inventor (given name family name)                                    |                       |
| Armin SCHMITT                                                                                      |                       |
| Signature<br>X                                                                                     | Date<br>X             |
| Residence<br>Berlin Germany                                                                        | Citizenship<br>German |
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| Full Name of additional joint inventor (given name family name)                                    |                       |
| Christian PILARSKY                                                                                 |                       |
| Signature<br>X   | Date<br>X 10.08.00    |
| Residence<br>Schönfeld Germany                                                                     | Citizenship<br>German |
| Post Office Address Heinrich-Lange-Strasse 13c, D-01474 Schönfeld, Germany                         |                       |
| Full Name of additional joint inventor (given name family name)                                    |                       |
| Edgar DAHL                                                                                         |                       |
| Signature<br>X  | Date<br>X 10.08.2000  |
| Residence<br>Potsdam Germany                                                                       | Citizenship<br>German |
| Post Office Address Eleonore-Procheska-Strasse 6, D-14480 Potsdam, Germany                         |                       |
| Full Name of additional joint inventor (given name family name)                                    |                       |
| André ROSENTHAL                                                                                    |                       |
| Signature<br>X  | Date<br>X 29/8/00     |
| Residence<br>Berlin Germany                                                                        | Citizenship<br>German |
| Post Office Address Koppenplatz 10, D-10115 Berlin, Germany                                        |                       |

☐ Additional joint inventors are named on separately numbered sheets attached hereto

## Sequence protocol

&lt;110&gt; metaGen Gesellschaft für Genomforschung mbH

&lt;120&gt; Human Nucleic Acid Sequences from Breast Tissue

&lt;130&gt; 51572AWOM1XX24-P

&lt;140&gt; PCT/DE99/00909

&lt;141&gt; 1999-03-19

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| tggcaccagt | tgaagtagag  | gaacttctaa  | gacaagcctc  | agagagaaac | tctaaatccc  | 240  |
| caacagagta | tcattgagcct | gtatatgccca | atccctttta  | caggcctaca | accccacaga  | 300  |
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| aacaagcaga | agagaagctt  | cacaccccg   | aaaaaaggct  | aatgactcct | tgggaagaat  | 540  |
| cgaatgtcat | gcaggacaaa  | gatgcaccct  | ctocaaagcc  | aaggctgagc | cccagagaga  | 600  |
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<400> 28

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| ggtggtatcc  | atttcagtc   | ccatcttctg  | ctttcagacc  | aagggtggact | tcacctcgtg  | 180  |
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| tgtgctctac  | ttccaatagc  | tttactggct  | ccacatgctc  | tatgtctgctc | tggggggccat | 300  |
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| agccagagag  | ctttgtcccc  | ggcctcctgg  | acacataggc  | cattatcctg  | tattcctttg  | 960  |
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<400> 29

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| agaaatgggt | ttctacaaag | atgcaaagac | tgctgcttct | ggaattccct  | accacagcga | 180 |
| ggtccctgtg | agtttgaaag | aagctgtctg | cgaagtggcc | cttgattaca  | aaaagaagaa | 240 |
| acacgtattc | aagctaagac | taaatgatgg | caatgagtac | ctcttccaag  | ccaaagacaa | 300 |
| aqagaacqcg | ttcagccttt | ttggcaaaaa | gaaatgaact | cctttccttc  | acctcctgcc | 360 |

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&lt;211&gt; 933

&lt;212&gt; DNA

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&lt;400&gt; 30

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<212> DNA

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<400> 34

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| gaccataaca | gccaacaggt  | ggcaggacca | ggactatagc | ccaggtcctc | tgatacccag | 180 |
| agcattacgt | gagccaggta  | atgagggact | ggaaccaggg | agaccgagcg | ctttctggaa | 240 |
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| tggtgctgtg | gccagggtga  | gagctgctct | ggaaaatgtg | acccagatcc | tcacaaccac | 540 |
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| cacaggcgct | gacagccgtc  | ccagcccttc | tgtctgcggg  | cctgaaccaa | acggtgccat | 180  |
| ggggaactgt | ctgcacaggg  | cggagtcttc | ccctcaactg  | agaactcaag | tcagctggac | 240  |
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| ctgccccttc | tcacccctac  | cagtgtcctg | ggtatcctag  | ctagcagcac | tgtcctcttc | 420  |
| atgcttttca | gacctctctt  | ccgctggcag | ctctgcccct  | gctggcctgt | cctggcacag | 480  |
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<213> homo sapiens

<400> 37

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| cacgcttggc  | aatgctgcag | aatgagttgg | aggggctggg | ggacatcttc | caccccatga  | 360 |
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| aacaggggag  | ctacttcggt | cgtttaggtg | acctgggtcc | cagcttccgc | cagcgggcat  | 480 |
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| agctccaggga | ctgcttcagg | ctgattgaaa | aggcccagca | ggctccagaa | gggcagccac  | 600 |



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&lt;211&gt; 2720

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 38

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&lt;210&gt; 41

&lt;211&gt; 2939

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 41

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&lt;211&gt; 3670

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 42

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| gacgccttc   | cggaggagta  | cgtgcccac  | gtcttcgac   | actacgcgt   | cagcgtcac   | 180  |
| tgggggggca  | agcagtaacct | cttaggactc | tatgacacgg  | cgggacagga  | agactatgac  | 240  |
| cgtctgaggc  | ctttatctta  | cccaatgacc | gatgtcttc   | ttatatgctt  | ctcggtggtta | 300  |
| aatccagcct  | catttcaaaa  | tgtgaaagag | gagtgggatc  | cggaaactta  | ggaataacca  | 360  |
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| gcaaaagaga  | taggagcatg  | ctgctatgtg | gaatgttcag  | ctttaaccca  | gaagggattg  | 540  |
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| aaaagaatatg | gatcaagatg  | tataaactgt | tgtttaatta  | cgtgagaaac  | atcttcatgt  | 660  |
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| agtttaaaaa  | gttacaatca  | ctcatgttg  | taactacgta  | aaaaacagag  | ctgtaaattgg | 960  |
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| ttcatctaca  | agcagttgg   | ccctaagtga | aaggctctgc  | ttgaaaaaaa  | aaagaaaaaa  | 1860 |
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<211> 615
<212> DNA
<213> homo sapiens

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```

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<211> 1488
<212> DNA
<213> homo sapiens

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<400> 51
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<212> DNA
<213> homo sapiens

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<400> 53

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<211> 1301
<212> DNA
<213> homo sapiens

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<400> 54

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&lt;400&gt; 55

000

&lt;210&gt; 56

&lt;211&gt; 1265

&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 56

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&lt;211&gt; 274

&lt;212&gt; DNA

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&lt;400&gt; 57

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<400> 59

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 <212> DNA  
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&lt;211&gt; 2313

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&lt;213&gt; homo sapiens

&lt;400&gt; 62

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<400> 63

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&lt;213&gt; homo sapiens

&lt;400&gt; 65

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<213> homo sapiens

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<211> 366
<212> PRT
<213> homo sapiens
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| 1997-1998 |  | 1998-1999 |  | 1999-2000 |  | 2000-2001 |  | 2001-2002 |  | 2002-2003 |  | 2003-2004 |  | 2004-2005 |  | 2005-2006 |  | 2006-2007 |  | 2007-2008 |  | 2008-2009 |  | 2009-2010 |  | 2010-2011 |  | 2011-2012 |  | 2012-2013 |  | 2013-2014 |  | 2014-2015 |  | 2015-2016 |  | 2016-2017 |  | 2017-2018 |  | 2018-2019 |  | 2019-2020 |  | 2020-2021 |  | 2021-2022 |  | 2022-2023 |  | 2023-2024 |  | 2024-2025 |  | 2025-2026 |  | 2026-2027 |  | 2027-2028 |  | 2028-2029 |  | 2029-2030 |  | 2030-2031 |  | 2031-2032 |  | 2032-2033 |  | 2033-2034 |  | 2034-2035 |  | 2035-2036 |  | 2036-2037 |  | 2037-2038 |  | 2038-2039 |  | 2039-2040 |  | 2040-2041 |  | 2041-2042 |  | 2042-2043 |  | 2043-2044 |  | 2044-2045 |  | 2045-2046 |  | 2046-2047 |  | 2047-2048 |  | 2048-2049 |  | 2049-2050 |  | 2050-2051 |  | 2051-2052 |  | 2052-2053 |  | 2053-2054 |  | 2054-2055 |  | 2055-2056 |  | 2056-2057 |  | 2057-2058 |  | 2058-2059 |  | 2059-2060 |  | 2060-2061 |  | 2061-2062 |  | 2062-2063 |  | 2063-2064 |  | 2064-2065 |  | 2065-2066 |  | 2066-2067 |  | 2067-2068 |  | 2068-2069 |  | 2069-2070 |  | 2070-2071 |  | 2071-2072 |  | 2072-2073 |  | 2073-2074 |  | 2074-2075 |  | 2075-2076 |  | 2076-2077 |  | 2077-2078 |  | 2078-2079 |  | 2079-2080 |  | 2080-2081 |  | 2081-2082 |  | 2082-2083 |  | 2083-2084 |  | 2084-2085 |  | 2085-2086 |  | 2086-2087 |  | 2087-2088 |  | 2088-2089 |  | 2089-2090 |  | 2090-2091 |  | 2091-2092 |  | 2092-2093 |  | 2093-2094 |  | 2094-2095 |  | 2095-2096 |  | 2096-2097 |  | 2097-2098 |  | 2098-2099 |  | 2099-2100 |  | 2100-2101 |  | 2101-2102 |  | 2102-2103 |  | 2103-2104 |  | 2104-2105 |  | 2105-2106 |  | 2106-2107 |  | 2107-2108 |  | 2108-2109 |  | 2109-2110 |  | 2110-2111 |  | 2111-2112 |  | 2112-2113 |  | 2113-2114 |  | 2114-2115 |  | 2115-2116 |  | 2116-2117 |  | 2117-2118 |  | 2118-2119 |  | 2119-2120 |  | 2120-2121 |  | 2121-2122 |  | 2122-2123 |  | 2123-2124 |  | 2124-2125 |  | 2125-2126 |  | 2126-2127 |  | 2127-2128 |  | 2128-2129 |  | 2129-2130 |  | 2130-2131 |  | 2131-2132 |  | 2132-2133 |  | 2133-2134 |  | 2134-2135 |  | 2135-2136 |  | 2136-2137 |  | 2137-2138 |  | 2138-2139 |  | 2139-2140 |  | 2140-2141 |  | 2141-2142 |  | 2142-2143 |  | 2143-2144 |  | 2144-2145 |  | 2145-2146 |  | 2146-2147 |  | 2147-2148 |  | 2148-2149 |  | 2149-2150 |  | 2150-2151 |  | 2151-2152 |  | 2152-2153 |  | 2153-2154 |  | 2154-2155 |  | 2155-2156 |  | 2156-2157 |  | 2157-2158 |  | 2158-2159 |  | 2159-2160 |  | 2160-2161 |  | 2161-2162 |  | 2162-2163 |  | 2163-2164 |  | 2164-2165 |  | 2165-2166 |  | 2166-2167 |  | 2167-2168 |  | 2168-2169 |  | 2169-2170 |  | 2170-2171 |  | 2171-2172 |  | 2172-2173 |  | 2173-2174 |  | 2174-2175 |  | 2175-2176 |  | 2176-2177 |  | 2177-2178 |  | 2178-2179 |  | 2179-2180 |  | 2180-2181 |  | 2181-2182 |  | 2182-2183 |  | 2183-2184 |  | 2184-2185 |  | 2185-2186 |  | 2186-2187 |  | 2187-2188 |  | 2188-2189 |  | 2189-2190 |  | 2190-2191 |  | 2191-2192 |  | 2192-2193 |  | 2193-2194 |  | 2194-2195 |  | 2195-2196 |  | 2196-2197 |  | 2197-2198 |  | 2198-2199 |  | 2199-2200 |  | 2200-2201 |  | 2201-2202 |  | 2202-2203 |  | 2203-2204 |  | 2204-2205 |  | 2205-2206 |  | 2206-2207 |  | 2207-2208 |  | 2208-2209 |  | 2209-2210 |  | 2210-2211 |  | 2211-2212 |  | 2212-2213 |  | 2213-2214 |  | 2214-2215 |  | 2215-2216 |  | 2216-2217 |  | 2217-2218 |  | 2218-2219 |  | 2219-2220 |  | 2220-2221 |  | 2221-2222 |  | 2222-2223 |  | 2223-2224 |  |
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&lt;400&gt; 77

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ile<br>1   | Ala        | Ser        | Ala        | Arg<br>5   | Leu        | Glu        | Glu        | Val        | Thr<br>10  | Gly        | Lys        | Leu        | Gln        | Val<br>15  | Ala        |
| Arg        | Asn        | Leu        | Ile<br>20  | Met        | Arg        | Gly        | Thr        | Glu<br>25  | Met        | Cys        | Pro        | Lys        | Ser<br>30  | Glu        | Asp        |
| Val        | Trp        | Leu<br>35  | Glu        | Ala        | Ala        | Arg        | Leu<br>40  | Gln        | Pro        | Gly        | Asp        | Thr<br>45  | Ala        | Lys        | Ala        |
| Val        | Val<br>50  | Ala        | Gln        | Ala        | Val        | Arg<br>55  | His        | Leu        | Pro        | Gln        | Ser<br>60  | Val        | Arg        | Ile        | Tyr        |
| Ile<br>65  | Arg        | Ala        | Ala        | Glu        | Leu<br>70  | Glu        | Thr        | Asp        | Ile        | Arg<br>75  | Ala        | Lys        | Lys        | Arg        | Val<br>80  |
| Leu        | Arg        | Lys        | Ala        | Leu<br>85  | Glu        | His        | Val        | Pro        | Asn<br>90  | Ser        | Val        | Arg        | Leu        | Trp<br>95  | Lys        |
| Ala        | Ala        | Val        | Glu<br>100 | Leu        | Glu        | Glu        | Pro        | Glu<br>105 | Asp        | Ala        | Arg        | Ile        | Met<br>110 | Leu        | Ser        |
| Arg        | Ala        | Val<br>115 | Glu        | Cys        | Cys        | Pro        | Thr<br>120 | Ser        | Val        | Glu        | Leu        | Trp<br>125 | Leu        | Ala        | Leu        |
| Ala        | Arg<br>130 | Leu        | Glu        | Thr        | Tyr        | Glu<br>135 | Asn        | Ala        | Arg        | Lys        | Val<br>140 | Leu        | Asn        | Lys        | Ala        |
| Arg<br>145 | Glu        | Asn        | Ile        | Pro        | Thr<br>150 | Asp        | Arg        | His        | Ile        | Trp<br>155 | Ile        | Thr        | Ala        | Ala        | Lys<br>160 |
| Leu        | Glu        | Glu        | Ala        | Asn<br>165 | Gly        | Asn        | Thr        | Gln        | Met<br>170 | Val        | Glu        | Lys        | Ile        | Ile<br>175 | Asp        |
| Arg        | Ala        | Ile        | Thr<br>180 | Ser        | Leu        | Arg        | Ala        | Asn<br>185 | Gly        | Val        | Glu        | Ile        | Asn<br>190 | Arg        | Glu        |
| Gln        | Trp        | Ile<br>195 | Gln        | Asp        | Ala        | Glu        | Glu<br>200 | Cys        | Asp        | Arg        | Ala        | Gly<br>205 | Ser        | Val        | Ala        |
| Thr        | Cys<br>210 | Gln        | Ala        | Val        | Met        | Arg<br>215 | Ala        | Val        | Ile        | Gly        | Ile<br>220 | Gly        | Ile        | Glu        | Glu        |
| Glu<br>225 | Asp        | Arg        | Lys        | His        | Thr<br>230 | Trp        | Met        | Glu        | Asp        | Ala<br>235 | Asp        | Ser        | Cys        | Val        | Ala<br>240 |
| His        | Asn        | Ala        | Leu        | Glu<br>245 | Cys        | Ala        | Arg        | Ala        | Ile<br>250 | Tyr        | Ala        | Tyr        | Ala        | Leu<br>255 | Gln        |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Pro | Ser | Leu | Gln | Ser | Lys | Thr | Lys | Asn | Asn | Lys | Trp | Ser | Cys |
| 1   |     |     |     | 5   |     | .   |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Met | Leu | Tyr | Cys | Phe | Ala | Gln | Asn |     |     |     |     |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Pro | Val | Ser | Thr | Lys | Gln | Asn | Glu | Lys | Gln | Gln | Met | Glu | Leu | Cys |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Val | Val | Leu | Leu | Cys | Thr | Lys | Leu | Gly | Thr | Gly | Val |     |     |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     |     |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Lys | Arg | Arg | Val | Ser | Asp | Thr | Ser | Ser | Gly | Pro | Thr | Pro | Cys | Met |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Pro | Ile | Leu | Gly | Arg | Thr | His | Tyr | Ser | Gln | Leu | Arg | Lys | Lys | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gly | Gln | Asp | Ser | His | Gln | His | Ile | Thr | His | Val | Leu | Leu | Gly | Arg |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Lys | Gln | Tyr | Ile | Pro | Val | Glu | Arg | Ser | Gln | Ser | Ile | Ser | Gly | Arg |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Val | Val | Lys | Gly | Gly | Arg | Cys | Tyr | Ala | Ala | Ala | Pro | Ser | Val | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Val | Ala | Val | Ile | Pro |     |     |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

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[illegible]

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[illegible]

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Asn Arg Gly Gly Val Gly Phe Gly Val Gly Trp Ser Leu Pro Phe Glu



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|           |           |           |           |     |           |           |           |           |     |     |           |           |           |     |     |
|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|-----|
| 1         |           |           |           | 5   |           |           | 43        |           | 10  |     |           |           | 15        |     |     |
| Leu       | Leu       | Ile       | Phe<br>20 | Met | Ser       | Arg       | Leu       | Gln<br>25 | Asn | Ser | Arg       | Val       | Gly<br>30 | Leu | Thr |
| Met       | Trp       | Gly<br>35 | Gly       | Gly | Gly       | Ser       | Ser<br>40 | Leu       | Phe | Phe | Tyr       | Phe<br>45 | Gln       | Val | His |
| Ser       | Trp<br>50 | Gly       | Trp       | Trp | Gly       | Gly<br>55 | Arg       | Arg       | Ile | Pro | Leu<br>60 | Pro       | Lys       | Pro | Leu |
| Val<br>65 | Cys       | Ala       | Glu       | Leu | Ala<br>70 | Leu       |           |           |     |     |           |           |           |     |     |

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|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Tyr<br>1 | Arg       | His       | Glu       | Pro<br>5 | Leu | Tyr       | Pro       | Ala       | Phe<br>10 | Pro | Tyr | Lys       | Ile       | Gln<br>15 | Arg |
| Glu      | Asn       | Phe       | Tyr<br>20 | Thr      | Phe | Ile       | Pro       | Gln<br>25 | Ile       | Lys | Gln | Val       | Leu<br>30 | Ser       | Ser |
| Tyr      | Arg       | Ala<br>35 | Leu       | Ala      | Arg | Ser       | Ile<br>40 | Cys       | Lys       | Arg | Asn | Leu<br>45 | Lys       | Phe       | Ser |
| Cys      | Arg<br>50 | Ile       | Lys       | Leu      | Asp | Lys<br>55 |           |           |           |     |     |           |           |           |     |

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| Leu<br>1  | Ala       | Thr       | His       | Ser<br>5 | Pro       | Gln       | Lys       | Ser       | His<br>10 | Gln       | Cys       | Ala       | His       | Cys<br>15 | Glu       |
| Lys       | Thr       | Phe       | Asn<br>20 | Arg      | Lys       | Asp       | His       | Leu<br>25 | Lys       | Asn       | His       | Leu       | Gln<br>30 | Thr       | His       |
| Asp       | Pro       | Asn<br>35 | Lys       | Met      | Ala       | Phe       | Gly<br>40 | Cys       | Glu       | Glu       | Cys       | Gly<br>45 | Lys       | Lys       | Tyr       |
| Asn       | Thr<br>50 | Met       | Leu       | Gly      | Tyr       | Lys<br>55 | Arg       | His       | Leu       | Ala       | Leu<br>60 | His       | Ala       | Ala       | Ser       |
| Ser<br>65 | Gly       | Asp       | Leu       | Thr      | Cys<br>70 | Gly       | Val       | Cys       | Ala       | Leu<br>75 | Glu       | Leu       | Gly       | Ser       | Thr<br>80 |
| Glu       | Val       | Leu       | Leu       | Asp      | His       | Leu       | Lys       | Ala       | His       | Ala       | Glu       | Glu       | Lys       | Pro       | Pro       |

000260" 6959460



|            |            |            |            | 85         | 44         |            |            |            | 90         | 95         |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ser        | Gly        | Thr        | Lys<br>100 | Glu        | Lys        | Lys        | His        | Gln<br>105 | Cys        | Asp        | His        | Cys        | Glu<br>110 | Arg        | Cys        |
| Phe        | Tyr        | Thr<br>115 | Arg        | Lys        | Asp        | Val        | Arg<br>120 | Arg        | His        | Leu        | Val        | Val<br>125 | His        | Thr        | Gly        |
| Cys        | Lys<br>130 | Asp        | Phe        | Leu        | Cys        | Gln<br>135 | Phe        | Cys        | Ala        | Gln        | Arg<br>140 | Phe        | Gly        | Arg        | Lys        |
| Asp<br>145 | His        | Leu        | Thr        | Arg        | His<br>150 | Thr        | Lys        | Lys        | Thr        | His<br>155 | Ser        | Gln        | Glu        | Leu        | Met<br>160 |
| Lys        | Glu        | Ser        | Leu        | Gln<br>165 | Thr        | Gly        | Asp        | Leu        | Leu<br>170 | Ser        | Thr        | Phe        | His        | Thr<br>175 | Ile        |
| Ser        | Pro        | Ser        | Phe<br>180 | Gln        | Leu        | Lys        | Ala        | Ala<br>185 | Ala        | Leu        | Pro        | Pro        | Phe<br>190 | Pro        | Leu        |
| Gly        | Ala        | Ser<br>195 | Ala        | Gln        | Asn        | Gly        | Leu<br>200 | Ala        | Ser        | Ser        | Leu        | Pro<br>205 | Ala        | Glu        | Val        |
| His        | Ser<br>210 | Leu        | Thr        | Leu        | Ser        | Pro<br>215 | Pro        | Glu        | Gln        | Ala        | Ala<br>220 | Gln        | Pro        | Met        | Gln        |
| Pro<br>225 | Leu        | Pro        | Glu        | Ser        | Leu<br>230 | Ala        | Ser        | Leu        | His        | Pro<br>235 | Ser        | Val        | Ser        | Pro        | Gly<br>240 |
| Ser        | Pro        | Pro        | Pro        | Pro<br>245 | Leu        | Pro        | Asn        | His        | Lys<br>250 | Tyr        | Asn        | Thr        | Thr        | Ser<br>255 | Thr        |
| Ser        | Tyr        | Ser        | Pro<br>260 | Leu        | Ala        | Ser        | Leu        | Pro<br>265 | Leu        | Lys        | Ala        | Asp        | Thr<br>270 | Lys        | Gly        |
| Phe        | Cys        | Asn<br>275 | Ile        | Ser        | Leu        | Phe        | Glu<br>280 | Asp        | Leu        | Pro        | Leu        | Gln<br>285 | Glu        | Pro        | Gln        |
| Ser        | Pro<br>290 | Gln        | Lys        | Leu        | Asn        | Pro<br>295 | Gly        | Phe        | Asp        | Leu        | Ala<br>300 | Lys        | Gly        | Asn        | Ala        |
| Gly<br>305 | Lys        | Val        | Asn        | Leu        | Pro<br>310 | Lys        | Glu        | Leu        | Pro        | Ala<br>315 | Asp        | Ala        | Val        | Asn        | Leu<br>320 |
| Thr        | Ile        | Pro        | Ala        | Ser<br>325 | Leu        | Asp        | Leu        | Ser        | Pro<br>330 | Leu        | Leu        | Gly        | Phe        | Trp<br>335 | Gln        |
| Leu        | Pro        | Pro        | Pro<br>340 | Ala        | Thr        | Gln        | Asn        | Thr<br>345 | Phe        | Gly        | Asn        | Ser        | Thr<br>350 | Leu        | Ala        |

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<213> homo sapiens
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|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Lys<br>1   | Arg        | Cys        | Gln        | Arg<br>5   | Lys        | Gln        | Pro        | Leu        | Arg<br>10  | Gly        | Ile        | Gly        | Ile        | Leu<br>15  | Lys        |
| Gln        | Ala        | Ile        | Asp<br>20  | Lys        | Met        | Gln        | Met        | Asn<br>25  | Thr        | Asn        | Gln        | Leu        | Thr<br>30  | Ser        | Ile        |
| His        | Ala        | Asp<br>35  | Leu        | Cys        | Gln        | Leu        | Cys<br>40  | Leu        | Leu        | Ala        | Lys        | Cys<br>45  | Phe        | Lys        | Pro        |
| Ala        | Leu<br>50  | Pro        | Tyr        | Leu        | Asp        | Val<br>55  | Asp        | Met        | Met        | Asp        | Ile<br>60  | Cys        | Lys        | Glu        | Asn        |
| Gly<br>65  | Ala        | Tyr        | Asp        | Ala        | Lys<br>70  | His        | Phe        | Leu        | Cys        | Tyr<br>75  | Tyr        | Tyr        | Tyr        | Gly        | Gly<br>80  |
| Met        | Ile        | Tyr        | Thr        | Gly<br>85  | Leu        | Lys        | Asn        | Phe        | Glu<br>90  | Arg        | Ala        | Leu        | Tyr        | Phe<br>95  | Tyr        |
| Glu        | Gln        | Ala        | Ile<br>100 | Thr        | Thr        | Pro        | Ala        | Met<br>105 | Ala        | Val        | Ser        | His        | Ile<br>110 | Met        | Leu        |
| Glu        | Ser        | Tyr<br>115 | Lys        | Lys        | Tyr        | Ile        | Leu<br>120 | Val        | Ser        | Leu        | Ile        | Leu<br>125 | Leu        | Gly        | Lys        |
| Val        | Gln<br>130 | Gln        | Leu        | Pro        | Lys        | Tyr<br>135 | Thr        | Ser        | Gln        | Ile        | Val<br>140 | Gly        | Arg        | Phe        | Ile        |
| Lys<br>145 | Pro        | Leu        | Ser        | Asn        | Ala<br>150 | Tyr        | His        | Glu        | Leu        | Ala<br>155 | Gln        | Val        | Tyr        | Ser        | Thr<br>160 |
| Asn        | Asn        | Pro        | Ser        | Glu<br>165 | Leu        | Arg        | Asn        | Leu        | Val<br>170 | Asn        | Lys        | His        | Ser        | Glu<br>175 | Thr        |

<400> 92

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Met<br>1   | Asp        | Leu        | Ser        | Leu<br>5   | Leu        | Trp        | Val<br>47  | Leu        | Leu<br>10  | Pro        | Leu        | Val        | Thr        | Met<br>15  | Ala        |
| Trp        | Gly        | Gln        | Tyr<br>20  | Gly        | Asp        | Tyr        | Gly        | Tyr<br>25  | Pro        | Tyr        | Gln        | Gln        | Tyr<br>30  | His        | Asp        |
| Tyr        | Ser        | Asp<br>35  | Asp        | Gly        | Trp        | Val        | Asn<br>40  | Leu        | Asn        | Arg        | Gln        | Gly<br>45  | Phe        | Ser        | Tyr        |
| Gln        | Cys<br>50  | Pro        | Gln        | Gly        | Gln        | Val<br>55  | Ile        | Val        | Ala        | Val        | Arg<br>60  | Ser        | Ile        | Phe        | Ser        |
| Lys<br>65  | Lys        | Glu        | Gly        | Ser        | Asp<br>70  | Arg        | Gln        | Trp        | Asn        | Tyr<br>75  | Ala        | Cys        | Met        | Pro        | Thr<br>80  |
| Pro        | Gln        | Ser        | Leu        | Gly<br>85  | Glu        | Pro        | Thr        | Glu        | Cys<br>90  | Trp        | Trp        | Glu        | Glu        | Ile<br>95  | Asn        |
| Arg        | Ala        | Gly        | Met<br>100 | Glu        | Trp        | Tyr        | Gln        | Thr<br>105 | Cys        | Ser        | Asn        | Asn        | Gly<br>110 | Leu        | Val        |
| Ala        | Gly        | Phe<br>115 | Gln        | Ser        | Arg        | Tyr        | Phe<br>120 | Glu        | Ser        | Val        | Leu        | Asp<br>125 | Arg        | Glu        | Trp        |
| Gln        | Phe<br>130 | Tyr        | Cys        | Cys        | Arg        | Tyr<br>135 | Ser        | Lys        | Arg        | Cys        | Pro<br>140 | Tyr        | Ser        | Cys        | Trp        |
| Leu<br>145 | Thr        | Thr        | Glu        | Tyr        | Pro<br>150 | Gly        | His        | Tyr        | Gly        | Glu<br>155 | Glu        | Met        | Asp        | Met        | Ile<br>160 |
| Ser        | Tyr        | Asn        | Tyr        | Asp<br>165 | Tyr        | Tyr        | Ile        | Arg        | Gly<br>170 | Ala        | Thr        | Thr        | Thr        | Phe<br>175 | Ser        |
| Ala        | Val        | Glu        | Arg<br>180 | Asp        | Arg        | Gln        | Trp        | Lys<br>185 | Phe        | Ile        | Met        | Cys        | Arg<br>190 | Met        | Thr        |
| Glu        | Tyr        | Asp<br>195 | Cys        | Glu        | Phe        | Ala        | Asn<br>200 | Val        |            |            |            |            |            |            |            |

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<213> homo sapiens
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<400> 93

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| Met<br>1 | Gly | Asn | Gly       | Leu<br>5 | Ser | Glu | Glu | Arg       | Gly<br>10 | Asn | Asn | Phe | Asn       | His<br>15 | Ile |
| Ser      | Pro | Ile | Pro<br>20 | Pro      | Val | Pro | His | Pro<br>25 | Arg       | Ser | Val | Ile | Gln<br>30 | Gln       | Ala |
| Glu      | Glu | Lys | Leu       | His      | Thr | Pro | Gln | Lys       | Arg       | Leu | Met | Thr | Pro       | Trp       | Glu |

0002269" 69554950

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     |     |     |     |     | 48  |     |     |     |     |     |     |     |  |
|     |     |     |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |  |
|     |     | 35  |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu | Ser | Asn | Val | Met | Gln | Asp | Lys | Asp | Ala | Pro | Ser | Pro | Lys | Pro | Arg |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Leu | Ser | Pro | Arg | Glu | Thr | Ile | Phe | Gly | Lys | Ser | Glu | His | Gln | Asn | Ser |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Ser | Pro | Thr | Cys | Gln | Glu | Asp | Glu | Glu | Asp | Val | Arg | Tyr | Asn | Ile | Val |  |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| His | Ser | Leu | Pro | Pro | Asp | Ile | Asn | Asp | Thr | Glu | Pro | Val | Thr | Met | Ile |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Phe | Met | Gly | Tyr | Gln | Gln | Ala | Glu | Asp | Ser | Glu | Glu | Asp | Lys | Lys | Phe |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Leu | Thr | Gly | Tyr | Asp | Gly | Ile | Ile | His | Ala | Glu | Leu | Val | Val | Ile | Asp |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Asp | Glu | Glu | Glu | Glu | Asp | Glu | Gly | Glu | Ala | Glu | Lys | Pro | Ser | Tyr | His |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Pro | Ile | Ala | Pro | His | Ser | Gln | Val | Tyr | Gln | Pro | Ala | Lys | Pro | Thr | Pro |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Leu | Pro | Arg | Lys | Arg | Ser | Glu | Ala | Ser | Pro | His | Glu | Asn | Thr | Asn | His |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Lys | Ser | Pro | His | Lys | Asn | Ser | Ile | Ser | Leu | Lys | Glu | Gln | Glu | Glu | Ser |  |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |  |
| Leu | Gly | Ser | Pro | Val | His | His | Ser | Pro | Phe | Asp | Ala | Gln | Thr | Thr | Gly |  |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |  |
| Asp | Gly | Thr | Glu | Asp | Pro | Ser | Leu | Thr | Ala | Leu | Arg | Met | Arg | Met | Ala |  |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |  |
| Lys | Leu | Gly | Lys | Lys | Val | Ile |     |     |     |     |     |     |     |     |     |  |
|     |     |     |     | 245 |     |     |     |     |     |     |     |     |     |     |     |  |

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<400> 94  
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<210> 95  
<211> 188  
<212> PRT  
<213> homo sapiens

<400> 95

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Val | Leu | Arg | Glu | Tyr | Leu | Met | Ser | Gly | Gly | Ile | Cys | Pro | Val |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ser | Arg | Asp | Thr | Ile | Asp | Tyr | Leu | Leu | Ser | Lys | Asn | Gly | Ser | Gly | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ile | Ile | Ile | Val | Val | Gly | Gly | Ala | Ala | Glu | Ser | Leu | Ser | Ser | Met |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Pro | Gly | Lys | Asn | Ala | Val | Thr | Leu | Arg | Asn | Arg | Lys | Gly | Phe | Val | Lys |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Ala | Leu | Arg | His | Gly | Ala | Asp | Leu | Val | Pro | Ile | Tyr | Ser | Phe | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Glu | Asn | Glu | Val | Tyr | Lys | Gln | Val | Ile | Phe | Glu | Glu | Gly | Ser | Trp | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Arg | Trp | Val | Gln | Lys | Lys | Phe | Gln | Lys | Tyr | Ile | Gly | Phe | Ala | Pro | Cys |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ile | Phe | His | Gly | Arg | Gly | Leu | Phe | Ser | Ser | Asp | Thr | Trp | Gly | Leu | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Pro | Tyr | Ser | Lys | Pro | Ile | Thr | Thr | Val | Val | Gly | Glu | Pro | Ile | Thr | Ile |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Pro | Lys | Leu | Glu | His | Pro | Thr | Gln | Gln | Asp | Ile | Asp | Leu | Tyr | His | Thr |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Tyr | Met | Glu | Ala | Leu | Val | Lys | Leu | Phe | Asp | Lys | His | Lys | Thr | Lys |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Phe | Gly | Leu | Pro | Glu | Thr | Glu | Val | Leu | Glu | Val | Asn |     |     |     |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     |     |     |     |

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 <213> homo sapiens

<400> 96

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gly | Ala | Gly | Thr | Gln | Pro | Gly | Pro | Leu | Leu | Lys | Lys | Pro | Tyr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Ile | Lys | Ile | Ser | Lys | Thr | Ser | Val | Asp | Gly | Asp | Pro | His | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Asp | Phe | Pro | Leu | Ser | Arg | Leu | Thr | Val | Cys | Phe | Asn | Ile | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Pro | Gly | Asp | Ile | Leu | Arg | Leu | Val | Ser | Asp | His | Arg | Asp | Ser |

000260" 69594960

| 50         |            |            |            |            | 55         |            |            |            |            | 60         |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gly<br>65  | Val        | Thr        | Val        | Asn        | Gly<br>70  | Glu        | Leu        | Ile        | Gly        | Ala<br>75  | Pro        | Ala        | Pro        | Pro        | Asn<br>80  |
| Gly        | His        | Lys        | Lys        | Gln<br>85  | Arg        | Thr        | Tyr        | Leu        | Arg<br>90  | Thr        | Ile        | Thr        | Ile        | Leu<br>95  | Ile        |
| Asn        | Lys        | Pro        | Glu<br>100 | Arg        | Ser        | Tyr        | Leu        | Glu<br>105 | Ile        | Thr        | Pro        | Ser        | Arg<br>110 | Val        | Ile        |
| Leu        | Asp        | Gly<br>115 | Gly        | Asp        | Arg        | Leu        | Val<br>120 | Leu        | Pro        | Cys        | Asn        | Gln<br>125 | Ser        | Val        | Val        |
| Val        | Gly<br>130 | Ser        | Trp        | Gly        | Leu        | Glu<br>135 | Val        | Ser        | Val        | Ser        | Ala<br>140 | Asn        | Ala        | Asn        | Val        |
| Thr<br>145 | Val        | Thr        | Ile        | Gln        | Gly<br>150 | Ser        | Ile        | Ala        | Phe        | Val<br>155 | Ile        | Leu        | Ile        | His        | Leu<br>160 |
| Tyr        | Lys        | Lys        | Pro        | Ala<br>165 | Pro        | Phe        | Gln        | Arg        | His<br>170 | His        | Leu        | Gly        | Phe        | Tyr<br>175 | Ile        |
| Ala        | Asn        | Ser        | Glu<br>180 | Gly        | Leu        | Ser        | Ser        | Asn<br>185 | Cys        | His        | Gly        | Leu        | Leu<br>190 | Gly        | Gln        |
| Phe        | Leu        | Asn<br>195 | Gln        | Asp        | Ala        | Arg        | Leu<br>200 | Thr        | Glu        | Asp        | Pro        | Ala<br>205 | Gly        | Pro        | Ser        |
| Gln        | Asn<br>210 | Leu        | Thr        | His        | Pro        | Leu<br>215 | Leu        | Leu        | Gln        | Val        | Gly<br>220 | Glu        | Gly        | Pro        | Glu        |
| Ala<br>225 | Val        | Leu        | Thr        | Val        | Lys<br>230 | Gly        | His        | Gln        | Val        | Pro<br>235 | Val        | Val        | Trp        | Lys        | Gln<br>240 |
| Arg        | Lys        | Ile        | Tyr        | Asn<br>245 | Gly        | Glu        | Glu        | Gln        | Ile<br>250 | Asp        | Cys        | Trp        | Phe        | Ala<br>255 | Arg        |
| Asn        | Asn        | Ala        | Ala<br>260 | Lys        | Leu        | Ile        | Asp        | Gly<br>265 | Glu        | Tyr        | Lys        | Asp        | Tyr<br>270 | Leu        | Ala        |
| Ser        | His        | Pro<br>275 | Phe        | Asp        | Thr        | Gly        | Met<br>280 | Thr        | Leu        | Gly        | Gln        | Gly<br>285 | Met        | Ser        | Arg        |
| Glu        | Leu<br>290 |            |            |            |            |            |            |            |            |            |            |            |            |            |            |

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 <212> PRT



| 1990-1991 |  | 1991-1992 |  | 1992-1993 |  | 1993-1994 |  | 1994-1995 |  | 1995-1996 |  | 1996-1997 |  | 1997-1998 |  | 1998-1999 |  | 1999-2000 |  | 2000-2001 |  | 2001-2002 |  | 2002-2003 |  | 2003-2004 |  | 2004-2005 |  | 2005-2006 |  | 2006-2007 |  | 2007-2008 |  | 2008-2009 |  | 2009-2010 |  | 2010-2011 |  | 2011-2012 |  | 2012-2013 |  | 2013-2014 |  | 2014-2015 |  | 2015-2016 |  | 2016-2017 |  | 2017-2018 |  | 2018-2019 |  | 2019-2020 |  | 2020-2021 |  | 2021-2022 |  | 2022-2023 |  | 2023-2024 |  | 2024-2025 |  | 2025-2026 |  | 2026-2027 |  | 2027-2028 |  | 2028-2029 |  | 2029-2030 |  | 2030-2031 |  | 2031-2032 |  | 2032-2033 |  | 2033-2034 |  | 2034-2035 |  | 2035-2036 |  | 2036-2037 |  | 2037-2038 |  | 2038-2039 |  | 2039-2040 |  | 2040-2041 |  | 2041-2042 |  | 2042-2043 |  | 2043-2044 |  | 2044-2045 |  | 2045-2046 |  | 2046-2047 |  | 2047-2048 |  | 2048-2049 |  | 2049-2050 |  | 2050-2051 |  | 2051-2052 |  | 2052-2053 |  | 2053-2054 |  | 2054-2055 |  | 2055-2056 |  | 2056-2057 |  | 2057-2058 |  | 2058-2059 |  | 2059-2060 |  | 2060-2061 |  | 2061-2062 |  | 2062-2063 |  | 2063-2064 |  | 2064-2065 |  | 2065-2066 |  | 2066-2067 |  | 2067-2068 |  | 2068-2069 |  | 2069-2070 |  | 2070-2071 |  | 2071-2072 |  | 2072-2073 |  | 2073-2074 |  | 2074-2075 |  | 2075-2076 |  | 2076-2077 |  | 2077-2078 |  | 2078-2079 |  | 2079-2080 |  | 2080-2081 |  | 2081-2082 |  | 2082-2083 |  | 2083-2084 |  | 2084-2085 |  | 2085-2086 |  | 2086-2087 |  | 2087-2088 |  | 2088-2089 |  | 2089-2090 |  | 2090-2091 |  | 2091-2092 |  | 2092-2093 |  | 2093-2094 |  | 2094-2095 |  | 2095-2096 |  | 2096-2097 |  | 2097-2098 |  | 2098-2099 |  | 2099-2100 |  | 2100-2101 |  | 2101-2102 |  | 2102-2103 |  | 2103-2104 |  | 2104-2105 |  | 2105-2106 |  | 2106-2107 |  | 2107-2108 |  | 2108-2109 |  | 2109-2110 |  | 2110-2111 |  | 2111-2112 |  | 2112-2113 |  | 2113-2114 |  | 2114-2115 |  | 2115-2116 |  | 2116-2117 |  | 2117-2118 |  | 2118-2119 |  | 2119-2120 |  | 2120-2121 |  | 2121-2122 |  | 2122-2123 |  | 2123-2124 |  | 2124-2125 |  | 2125-2126 |  | 2126-2127 |  | 2127-2128 |  | 2128-2129 |  | 2129-2130 |  | 2130-2131 |  | 2131-2132 |  | 2132-2133 |  | 2133-2134 |  | 2134-2135 |  | 2135-2136 |  | 2136-2137 |  | 2137-2138 |  | 2138-2139 |  | 2139-2140 |  | 2140-2141 |  | 2141-2142 |  | 2142-2143 |  | 2143-2144 |  | 2144-2145 |  | 2145-2146 |  | 2146-2147 |  | 2147-2148 |  | 2148-2149 |  | 2149-2150 |  | 2150-2151 |  | 2151-2152 |  | 2152-2153 |  | 2153-2154 |  | 2154-2155 |  | 2155-2156 |  | 2156-2157 |  | 2157-2158 |  | 2158-2159 |  | 2159-2160 |  | 2160-2161 |  | 2161-2162 |  | 2162-2163 |  | 2163-2164 |  | 2164-2165 |  | 2165-2166 |  | 2166-2167 |  | 2167-2168 |  | 2168-2169 |  | 2169-2170 |  | 2170-2171 |  | 2171-2172 |  | 2172-2173 |  | 2173-2174 |  | 2174-2175 |  | 2175-2176 |  | 2176-2177 |  | 2177-2178 |  | 2178-2179 |  | 2179-2180 |  | 2180-2181 |  | 2181-2182 |  | 2182-2183 |  | 2183-2184 |  | 2184-2185 |  | 2185-2186 |  | 2186-2187 |  | 2187-2188 |  | 2188-2189 |  | 2189-2190 |  | 2190-2191 |  | 2191-2192 |  | 2192-2193 |  | 2193-2194 |  | 2194-2195 |  | 2195-2196 |  | 2196-2197 |  | 2197-2198 |  | 2198-2199 |  | 2199-2200 |  | 2200-2201 |  | 2201-2202 |  | 2202-2203 |  | 2203-2204 |  | 2204-2205 |  | 2205-2206 |  | 2206-2207 |  | 2207-2208 |  | 2208-2209 |  | 2209-2210 |  | 2210-2211 |  | 2211-2212 |  | 2212-2213 |  | 2213-2214 |  | 2214-2215 |  | 2215-2216 |  | 2216-2217 |  |
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Ser

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| Met<br>1  | Gly       | Lys       | Gly        | Leu<br>5  | Gly       | Glu       | Asp       | Gly        | Gln<br>10 | Gln       | Arg       | Ala       | Arg        | Glu<br>15 | Ser       |
| Trp       | Thr       | Ser       | Gln<br>20  | Arg       | Arg       | Arg       | Pro       | Gln<br>25  | Gln       | Val       | Gln       | Ser       | Arg<br>30  | Ala       | Ala       |
| Thr       | Ser       | Cys<br>35 | Pro        | Ala       | Gly       | Cys       | Leu<br>40 | Glu        | Gly       | Arg       | Gly       | Gln<br>45 | Arg        | Arg       | Val       |
| Met       | Ser<br>50 | Leu       | Gln        | Leu       | Gly       | Glu<br>55 | Gly       | Pro        | Ser       | Glu       | Leu<br>60 | His       | Val        | Ala       | Phe       |
| Ser<br>65 | Gln       | Arg       | Glu        | Gln       | Glu<br>70 | Gly       | Arg       | Ile        | Gly       | Arg<br>75 | Glu       | Asn       | Asn        | Gly       | Glu<br>80 |
| Gly       | Thr       | Cys       | Glu        | Gly<br>85 | Lys       | Gln       | Gly       | Gly        | Ser<br>90 | Glu       | Arg       | Phe       | Asp        | Gln<br>95 | Pro       |
| Ala       | Ile       | Thr       | Val<br>100 | Phe       | Trp       | Leu       | Ser       | Tyr<br>105 | Leu       | Ala       | Arg       | Arg       | Leu<br>110 | Arg       | Asp       |

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145

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| Met<br>1 | Arg | Thr | His       | Val<br>5 | Leu | Cys | Tyr | His       | Trp<br>10 | Pro | Arg | Lys | Arg       | Glu<br>15 | Ser |
| Gln      | Asp | Ser | Arg<br>20 | Ala      | Trp | Thr | Trp | Gly<br>25 | Lys       | Gly | Leu | Leu | Trp<br>30 | Asp       | Ser |
| Ala      | Pro | Gln | Pro       | Leu      | Gly | Gly | Pro | Arg       | Val       | Trp | Gly | Gln | Asp       | Trp       | Val |

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| Ser<br>1 | Glu       | Ala       | Arg       | Asn<br>5 | Ala | Pro       | Ser       | Gly       | Thr<br>10 | Ala | Gln       | Thr       | Phe       | Ala<br>15 | Met |
| Gly      | Phe       | Met       | Thr<br>20 | Gly      | Thr | Ile       | Ser       | Ser<br>25 | Met       | Tyr | Gln       | Thr       | Lys<br>30 | Ala       | Val |
| Ile      | Ile       | Ala<br>35 | Met       | Ile      | Ile | Thr       | Ala<br>40 | Val       | Val       | Ser | Ile       | Ser<br>45 | Val       | Thr       | Ile |
| Phe      | Cys<br>50 | Phe       | Gln       | Thr      | Lys | Val<br>55 | Asp       | Phe       | Thr       | Ser | Cys<br>60 | Thr       | Gly       | Leu       | Phe |
| Cys      | Val       | Leu       | Gly       | Ile      | Val | Leu       | Leu       | Val       | Thr       | Gly | Ile       | Val       | Thr       | Ser       | Ile |

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|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----|------------|------------|------------|-----------|-----|--|--|----|
| 65         |            |            |            |           |            | 70         |            |            | 55        |     |            |            |            |           | 75  |  |  | 80 |
| Val        | Leu        | Tyr        | Phe        | Gln<br>85 | Tyr        | Val        | Tyr        | Trp        | Leu<br>90 | His | Met        | Leu        | Tyr        | Ala<br>95 | Ala |  |  |    |
| Leu        | Gly        | Ala        | Ile<br>100 | Cys       | Phe        | Thr        | Leu        | Phe<br>105 | Leu       | Ala | Tyr        | Asp        | Thr<br>110 | Gln       | Leu |  |  |    |
| Val        | Leu        | Gly<br>115 | Asn        | Arg       | Lys        | His        | Thr<br>120 | Ile        | Ser       | Pro | Glu        | Asp<br>125 | Tyr        | Ile       | Thr |  |  |    |
| Gly        | Ala<br>130 | Leu        | Gln        | Ile       | Tyr        | Thr<br>135 | Asp        | Ile        | Ile       | Tyr | Ile<br>140 | Phe        | Thr        | Phe       | Val |  |  |    |
| Leu<br>145 | Gln        | Leu        | Met        | Gly       | Asp<br>150 | Arg        | Asn        |            |           |     |            |            |            |           |     |  |  |    |

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| <400> 105 |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |  |  |
| His<br>1  | Leu       | Leu       | Ser       | Pro<br>5 | Pro | His       | Ile       | Leu       | Gly<br>10 | Thr | Ala       | Phe       | Ser       | Ser<br>15 | Thr |  |  |
| Gly       | Asn       | Gly       | Thr<br>20 | Asp      | Gly | Gln       | Lys       | Thr<br>25 | Ser       | Ile | Thr       | Phe       | Met<br>30 | Lys       | Gly |  |  |
| Leu       | Leu       | Glu<br>35 | Leu       | Pro      | Gly | Lys       | Lys<br>40 | Ala       | Cys       | Leu | Gly       | Glu<br>45 | Leu       | Gly       | Arg |  |  |
| Cys       | Arg<br>50 | Gln       | Cys       | Gly      | Trp | Ala<br>55 | Gly       | Gly       | Gln       | Pro | Val<br>60 | Val       | Leu       | Leu       | Pro |  |  |
| Ala<br>65 | Gln       |           |           |          |     |           |           |           |           |     |           |           |           |           |     |  |  |

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 <212> PRT  
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| <400> 106 |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |  |  |
| Pro<br>1  | Thr | Ser       | Leu       | Ile<br>5 | Trp | Pro | Thr       | Thr       | Met<br>10 | Phe | Cys | Ser       | Val       | His<br>15 | Val |  |  |
| Leu       | Phe | Lys       | Ser<br>20 | Ile      | Leu | Asn | Trp       | Leu<br>25 | Pro       | Ser | Phe | Lys       | Leu<br>30 | Asn       | Gln |  |  |
| Thr       | Leu | Lys<br>35 | Ala       | Trp      | Ser | Ser | His<br>40 | Thr       | Gly       | Pro | Thr | Phe<br>45 | Pro       | His       | Gly |  |  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Tyr | Glu | Arg | Ala | Pro | Ala | Gln | Gln | Gly | Leu | Ser | Arg | Ser | Leu | Pro |
|     | 50  |     |     |     |     | 55  | 56  |     |     |     | 60  |     |     |     |     |
| Pro | Pro | Leu | Pro | Val | Pro | Gln | Ile | Trp | Pro | Leu | Leu | Arg | Lys | Ile | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Thr | Ala | Thr | Gly | Pro | Ser | Glu | Pro | Lys | Pro | Thr |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |     |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Pro | Ser | Phe | Phe | Leu | His | Phe | Ser | Leu | Ser | Ile | Tyr | Phe | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| His | Pro | Thr | Phe | Leu | Glu | Gln | Pro | Leu | Val | Leu | Gln | Glu | Met | Ala | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Asp | Arg | Arg | Leu | Ala | Leu | Pro | Ser |     |     |     |     |     |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     |     |     |     |     |

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<400> 108

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| Asn | Glu | Leu | Lys | Ala | Ser | Gly | Gly | Glu | Ile | Lys | Ile | His | Lys | Met | Glu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Lys | Glu | Asn | Val | Pro | Pro | Gly | Pro | Glu | Val | Cys | Ile | Thr | His | Gln |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Gly | Glu | Lys | Ile | Ser | Ala | Asn | Glu | Asn | Ser | Leu | Ala | Val | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Pro | Ala | Glu | Asp | Asp | Ser | Arg | Asp | Ser | Gln | Val | Lys | Ser | Glu | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gln | Gln | Pro | Val | His | Pro | Lys | Pro | Leu | Ser | Pro | Asp | Ser | Arg | Ala | Ser |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ser | Leu | Ser | Glu | Ser | Ser | Pro | Pro | Lys | Ala | Met | Lys | Lys | Phe | Gln | Ala |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Pro | Ala | Arg | Glu | Thr | Cys | Val | Glu | Cys | Gln | Lys | Thr | Val | Tyr | Pro | Met |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Arg | Leu | Leu | Ala | Asn | Gln | Gln | Val | Phe | His | Ile | Ser | Cys | Phe | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

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|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Cys        | Ser<br>130 | Tyr        | Cys        | Asn        | Asn        | Lys<br>135 | Leu        | Ser        | Leu        | Gly        | Thr<br>140 | Tyr        | Ala        | Ser        | Leu        |
| His<br>145 | Gly        | Arg        | Ile        | Tyr        | Cys<br>150 | Lys        | Pro        | His        | Phe        | Asn<br>155 | Gln        | Leu        | Phe        | Lys        | Ser<br>160 |
| Lys        | Gly        | Asn        | Tyr        | Asp<br>165 | Glu        | Gly        | Phe        | Gly        | His<br>170 | Arg        | Pro        | His        | Lys        | Asp<br>175 | Leu        |
| Trp        | Ala        | Ser        | Lys<br>180 | Asn        | Glu        | Asn        | Glu        | Glu<br>185 | Ile        | Leu        | Glu        | Arg        | Pro<br>190 | Ala        | Gln        |
| Leu        | Ala        | Asn<br>195 | Ala        | Arg        | Glu        | Thr        | Pro<br>200 | His        | Ser        | Pro        | Gly        | Val<br>205 | Glu        | Asp        | Ala        |
| Pro        | Ile<br>210 | Ala        | Lys        | Gly        | Gly        | Val<br>215 | Leu        | Ala        | Ala        | Ser        | Met<br>220 | Glu        | Ala        | Lys        | Ala        |
| Ser<br>225 | Ser        | Gln        | Gln        | Glu        | Lys<br>230 | Glu        | Asp        | Lys        | Pro        | Ala<br>235 | Glu        | Thr        | Lys        | Lys        | Leu<br>240 |
| Arg        | Ile        | Ala        | Trp        | Pro<br>245 | Pro        | Pro        | Thr        | Glu        | Leu<br>250 | Gly        | Ser        | Ser        | Gly        | Ser<br>255 | Ala        |
| Leu        | Glu        | Glu        | Gly<br>260 | Ile        | Lys        | Met        | Ser        | Lys<br>265 | Pro        | Lys        | Trp        | Pro        | Pro<br>270 | Glu        | Asp        |
| Glu        | Ile        | Ser<br>275 | Lys        | Pro        | Glu        | Val        | Pro<br>280 | Glu        | Asp        | Val        | Asp        | Leu<br>285 | Asp        | Leu        | Lys        |
| Lys        | Leu<br>290 | Arg        | Arg        | Ser        | Ser        | Ser<br>295 | Leu        | Lys        | Glu        | Arg        | Ser<br>300 | Arg        | Pro        | Phe        | Thr        |
| Val<br>305 | Ala        | Ala        | Ser        | Phe        | Gln<br>310 | Ser        | Thr        | Ser        | Val        | Lys<br>315 | Ser        | Pro        | Lys        | Thr        | Val<br>320 |
| Ser        | Pro        | Pro        | Ile        | Arg<br>325 | Lys        | Gly        | Trp        | Ser        | Met<br>330 | Ser        | Glu        | Gln        | Ser        | Glu<br>335 | Glu        |
| Ser        | Val        | Gly        | Gly<br>340 | Arg        | Val        | Ala        | Glu        | Arg<br>345 | Lys        | Gln        | Val        | Glu        | Asn<br>350 | Ala        | Lys        |
| Ala        | Ser        | Lys<br>355 | Lys        | Asn        | Gly        | Asn        | Val<br>360 | Gly        | Lys        | Thr        | Thr        | Trp<br>365 | Gln        | Asn        | Lys        |
| Glu        | Ser<br>370 | Lys        | Gly        | Glu        | Thr        | Gly<br>375 | Lys        | Arg        | Ser        | Lys        | Glu<br>380 | Gly        | His        | Ser        | Leu        |

Glu Met Glu Asn Glu Asn Leu Val<sup>58</sup> Glu Asn Gly Ala Asp Ser Asp Glu  
 385 390 395 400  
 Asp Asp Asn Ser Phe Leu Lys Gln Gln Ser Pro Gln Glu Pro Lys Ser  
 405 410 415  
 Leu Asn Trp Ser Ser Phe Val Asp Asn Thr Phe Ala Glu Glu Phe Thr  
 420 425 430  
 Thr Gln Asn Gln Lys Ser Gln Asp Val Glu Leu Trp Glu Gly Glu Val  
 435 440 445  
 Val Lys Glu Leu Ser Val Glu Glu Gln Ile Lys Arg Asn Arg Tyr Tyr  
 450 455 460

Asp Glu Asp Glu Asp Glu Glu  
 465 470

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<210> 111  
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<210> 112  
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 <212> PRT  
 <213> homo sapiens

<400> 112

Arg Lys Met Leu Arg Ala Ala Leu Pro Ala Leu Pro Ile Pro Arg Cys  
 1 5 10 15  
 Lys Tyr Thr Leu Phe Leu Ile Ala His Met Gly Pro Pro Tyr Leu Leu  
 20 25 30  
 Ala Leu Val Leu Met Leu Lys Ser Trp Pro Trp Glu Arg Cys Leu Pro  
 35 40 45  
 Gly Arg His Ser Cys Leu Val Gln Ala Lys Pro Leu Cys Asn Ala Ser  
 50 55 60  
 Pro Phe Trp Cys Tyr Glu Val Pro Leu Cys Arg Arg Phe His Gln Gln  
 65 70 75 80  
 Leu Val Thr Val Pro Ser Thr Arg Thr Cys Phe Glu Ile Ser  
 85 90

<210> 113

0002250" 69594960





|            |            |            |            |            |            |            |                   |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val        | Ser        | Ser        | Leu        | Gln<br>245 | Gly        | Leu        | Pro <sup>60</sup> | Ala        | Glu<br>250 | Leu        | Gln        | Gln        | Pro        | Val<br>255 | Gly        |
| Arg        | Ala        | Arg        | His<br>260 | Ser        | Leu        | Cys        | Glu               | Leu<br>265 | Tyr        | Gly        | Ile        | Val        | Ala<br>270 | Ser        | Ala        |
| Gly        | Ser        | Val<br>275 | Glu        | Glu        | Leu        | Pro        | Ala<br>280        | Glu        | Arg        | Leu        | Val        | Gln<br>285 | Ser        | Arg        | Glu        |
| Gly        | Val<br>290 | His        | Gln        | Ala        | Trp        | Gln<br>295 | Gly               | Leu        | Glu        | Gln        | Leu<br>300 | Leu        | Glu        | Gly        | Leu        |
| Gln<br>305 | His        | Asn        | Pro        | Pro        | Leu<br>310 | Ser        | Trp               | Leu        | Val        | Gly<br>315 | Pro        | Phe        | Ala        | Leu        | Pro<br>320 |

Ala Gly Gly Gln

<210> 114  
 <211> 148  
 <212> PRT  
 <213> homo sapiens

<400> 114

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Ile<br>1  | Ala        | Met        | Thr        | Pro<br>5  | Pro       | Asn        | Ala        | Thr        | Glu<br>10 | Ala       | Ser        | Lys        | Pro        | Gln<br>15 | Gly       |
| Thr       | Thr        | Val        | Cys<br>20  | Pro       | Pro       | Cys        | Asp        | Asn<br>25  | Glu       | Leu       | Lys        | Ser        | Glu<br>30  | Ala       | Ile       |
| Ile       | Glu        | His<br>35  | Leu        | Cys       | Ala       | Ser        | Glu<br>40  | Phe        | Ala       | Leu       | Arg        | Met<br>45  | Lys        | Ile       | Lys       |
| Glu       | Val<br>50  | Lys        | Lys        | Glu       | Asn       | Gly<br>55  | Asp        | Lys        | Lys       | Ile       | Val<br>60  | Pro        | Lys        | Lys       | Lys       |
| Lys<br>65 | Pro        | Leu        | Lys        | Leu       | Gly<br>70 | Pro        | Ile        | Lys        | Lys       | Lys<br>75 | Asp        | Leu        | Lys        | Lys       | Leu<br>80 |
| Val       | Leu        | Tyr        | Leu        | Lys<br>85 | Asn       | Gly        | Ala        | Asp        | Cys<br>90 | Pro       | Cys        | His        | Gln        | Leu<br>95 | Asp       |
| Asn       | Leu        | Ser        | His<br>100 | His       | Phe       | Leu        | Ile        | Met<br>105 | Gly       | Arg       | Lys        | Val        | Lys<br>110 | Ser       | Gln       |
| Tyr       | Leu        | Leu<br>115 | Thr        | Ala       | Ile       | His        | Lys<br>120 | Trp        | Asp       | Lys       | Lys        | Asn<br>125 | Lys        | Glu       | Phe       |
| Lys       | Asn<br>130 | Phe        | Met        | Lys       | Lys       | Met<br>135 | Lys        | Asn        | His       | Glu       | Cys<br>140 | Pro        | Thr        | Phe       | Gln       |
| Ser       | Val        | Phe        | Lys        |           |           |            |            |            |           |           |            |            |            |           |           |

000260"65594960

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<211> 45
<212> PRT
<213> homo sapiens
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|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Pro<br>1 | Val | Ile       | Tyr       | Ser<br>5 | Val | Leu | Ile       | Arg       | Ser<br>10 | Glu | Ile | Arg       | Tyr       | Lys<br>15 | Ile |
| Ser      | Arg | Pro       | Val<br>20 | Thr      | Thr | Asp | Phe       | Ile<br>25 | Lys       | Ser | Glu | Ser       | Leu<br>30 | Ile       | Leu |
| Ala      | Cys | Leu<br>35 | Tyr       | Leu      | Ile | Ser | Glu<br>40 | Arg       | Met       | Ser | Thr | Leu<br>45 |           |           |     |

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<212> PRT
<213> homo sapiens
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| Pro<br>1 | Asp | Cys       | Glu       | Ser<br>5 | Phe | Met | Tyr       | Phe       | Asn<br>10 | Leu | Asp | Ser | Val       | Phe<br>15 | Leu |
| Arg      | Val | Leu       | Ser<br>20 | Met      | Lys | Leu | Ala       | Asp<br>25 | Ser       | Arg | Gln | Asp | Ser<br>30 | Phe       | Phe |
| His      | His | Gly<br>35 | Trp       | Leu      | Ile | Ser | Pro<br>40 |           |           |     |     |     |           |           |     |

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<211> 27
<212> PRT
<213> homo sapiens
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|----------|-----|-----|-----------|----------|-----|-----|-----|-----------|-----------|-----|-----|-----|-----|-----------|-----|
| Thr<br>1 | Asn | Glu | His       | Thr<br>5 | Leu | Thr | Ser | Tyr       | Leu<br>10 | Gln | Leu | Pro | Phe | Ser<br>15 | Phe |
| Asn      | Arg | Ile | Val<br>20 | Lys      | Ala | Ser | Cys | Ile<br>25 | Leu       | Ile |     |     |     |           |     |

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<210> 118
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<210> 119
<211> 135
<212> PRT
<213> homo sapiens
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|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Arg<br>1 | Ser | Asn | Ala | Val<br>5 | Gln | Leu | Thr | Arg | Met<br>10 | Glu | Tyr | Ala | Met | Lys<br>15 | Ser |
| Leu      | Ser | Leu | Leu | Tyr      | Pro | Lys | Ser | Leu | Ser       | Arg | His | Val | Ser | Val       | Arg |

000260" 092000

|       |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|       |              |     |     | 20  |     |     |     | 62  |     | 25  |     |     |     | 30  |     |  |
| Thr   | Ser          | Val | Val | Thr | Gln | Gln | Leu | Leu | Ser | Glu | Pro | Ser | Pro | Lys | Ala |  |
|       |              | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Pro   | Arg          | Ala | Arg | Pro | Cys | Arg | Val | Ser | Thr | Ala | Asp | Arg | Ser | Val | Arg |  |
|       | 50           |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Lys   | Gly          | Ile | Met | Ala | Tyr | Ser | Leu | Glu | Asp | Leu | Leu | Leu | Lys | Val | Arg |  |
| 65    |              |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Asp   | Thr          | Leu | Met | Leu | Ala | Asp | Lys | Pro | Phe | Phe | Leu | Val | Leu | Glu | Glu |  |
|       |              |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Asp   | Gly          | Thr | Thr | Val | Glu | Thr | Glu | Glu | Tyr | Phe | Gln | Ala | Leu | Ala | Gly |  |
|       |              |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp   | Thr          | Val | Phe | Met | Val | Leu | Gln | Lys | Gly | Gln | Lys | Trp | Gln | Pro | Pro |  |
|       |              | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ser   | Glu          | Gln | Gly | Thr | Arg | His |     |     |     |     |     |     |     |     |     |  |
|       | 130          |     |     |     |     | 135 |     |     |     |     |     |     |     |     |     |  |
| <210> | 120          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <400> | 120          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 000   |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <210> | 121          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <400> | 121          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 000   |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <210> | 122          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <211> | 193          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <212> | PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <213> | homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <400> | 122          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu   | Ala          | Cys | Ala | His | Thr | Leu | Ser | Cys | Pro | Ala | Leu | Ala | Arg | Leu | Gly |  |
| 1     |              |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Arg   | Ala          | Arg | Arg | Arg | Pro | Trp | Met | Ser | His | Arg | Thr | Ser | Ser | Thr | Phe |  |
|       |              |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Arg   | Ala          | Glu | Arg | Ser | Phe | His | Ser | Ser | Ser | Ser | Ser | Ser | Ser | Ala | Ala |  |
|       |              | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Thr   | Ser          | Ser | Ser | Ala | Ser | Arg | Ala | Leu | Pro | Ala | Gln | Asp | Pro | Pro | Met |  |
|       | 50           |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Glu   | Lys          | Ala | Leu | Ser | Met | Phe | Ser | Asp | Asp | Phe | Gly | Ser | Phe | Met | Arg |  |
| 65    |              |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Pro   | His          | Ser | Glu | Pro | Leu | Ala | Phe | Pro | Ala | Arg | Pro | Gly | Gly | Ala | Gly |  |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|     |     |     |     | 85  |     |     | 63  |     | 90  |     |     |     | 95  |     |     |  |
| Asn | Ile | Lys | Thr | Leu | Gly | Asp | Ala | Tyr | Glu | Phe | Ala | Val | Asp | Val | Arg |  |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Asp | Phe | Ser | Pro | Glu | Asp | Ile | Ile | Val | Thr | Thr | Ser | Asn | Asn | His | Ile |  |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Glu | Val | Arg | Ala | Glu | Lys | Leu | Ala | Ala | Asp | Gly | Thr | Val | Met | Asn | Thr |  |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Phe | Ala | His | Lys | Cys | Gln | Leu | Pro | Glu | Asp | Val | Asp | Pro | Thr | Ser | Val |  |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Thr | Ser | Ala | Leu | Arg | Glu | Asp | Gly | Ser | Leu | Thr | Ile | Arg | Ala | Arg | Arg |  |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| His | Pro | His | Thr | Glu | His | Val | Gln | Gln | Thr | Phe | Arg | Thr | Glu | Ile | Lys |  |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |

Ile

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<400> 123  
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<210> 124  
<211> 38  
<212> PRT  
<213> homo sapiens

<400> 124

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Thr | Phe | Tyr | Pro | Leu | Phe | Pro | Asn | Gly | Gly | Gly | Thr | Tyr | Pro |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Glu | Val | Val | Asn | Asp | Phe | Pro | Leu | Lys | Leu | Leu | Tyr | Phe | Thr | Asn | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |

|     |     |     |     |     |     |  |  |  |  |  |  |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|--|--|--|--|
| Asn | Tyr | Phe | Val | Leu | Met |  |  |  |  |  |  |  |  |  |  |  |
|     |     | 35  |     |     |     |  |  |  |  |  |  |  |  |  |  |  |

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<212> PRT  
<213> homo sapiens

<400> 125

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Trp | Leu | Phe | His | Asp | Ala | Gly | Ile | Arg | Ser | Ala | Gly | Gly | Leu | Ser |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Leu | Leu | Ser | Cys | Gly | Ser | Trp | Pro | Leu | Pro | Ser | Gly | Tyr | His | Arg | Leu |  |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Gln | Asp | Thr | Asn | Gly | Gln | Gln | Lys | Asn | Val | Thr | Leu | Leu | Ile | Leu | Ser |  |

|       |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-------|--------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
|       |              |     |     |     |     |     | 64  |     |     |     |     |     |     |     |     |  |
|       |              |     |     |     |     |     | 40  |     |     |     |     |     | 45  |     |     |  |
| Ser   | Ser          | Ser | Ile | Gly | Thr | Lys | Leu | Pro | Ser | Arg | Pro | Arg | Glu | Ile | Leu |  |
|       | 50           |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| Cys   |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| 65    |              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <210> | 126          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <211> | 250          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <212> | PRT          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <213> | homo sapiens |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| <400> | 126          |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| Glu   | Thr          | Arg | Val | Lys | Thr | Ser | Leu | Glu | Leu | Leu | Arg | Thr | Gln | Leu | Glu |  |
| 1     |              |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |
| Pro   | Thr          | Gly | Thr | Val | Gly | Asn | Thr | Ile | Met | Thr | Ser | Gln | Pro | Val | Pro |  |
|       |              |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |
| Asn   | Glu          | Thr | Ile | Ile | Val | Leu | Pro | Ser | Asn | Val | Ile | Asn | Phe | Ser | Gln |  |
|       |              | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |
| Ala   | Glu          | Lys | Pro | Glu | Pro | Thr | Asn | Gln | Gly | Gln | Asp | Ser | Leu | Lys | Lys |  |
|       | 50           |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |
| His   | Leu          | His | Ala | Glu | Ile | Lys | Val | Ile | Gly | Thr | Ile | Gln | Ile | Leu | Cys |  |
| 65    |              |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |  |
| Gly   | Met          | Met | Val | Leu | Ser | Leu | Gly | Ile | Ile | Leu | Ala | Ser | Ala | Ser | Phe |  |
|       |              |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |  |
| Ser   | Pro          | Asn | Phe | Thr | Gln | Val | Thr | Ser | Thr | Leu | Leu | Asn | Ser | Ala | Tyr |  |
|       |              |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |  |
| Pro   | Phe          | Ile | Gly | Pro | Phe | Phe | Phe | Ile | Ile | Ser | Gly | Ser | Leu | Ser | Ile |  |
|       |              | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |  |
| Ala   | Thr          | Glu | Lys | Arg | Leu | Thr | Lys | Leu | Leu | Val | His | Ser | Ser | Leu | Val |  |
|       | 130          |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |  |
| Gly   | Ser          | Ile | Leu | Ser | Ala | Leu | Ser | Ala | Leu | Val | Gly | Phe | Ile | Ile | Leu |  |
| 145   |              |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |  |
| Ser   | Val          | Lys | Gln | Ala | Thr | Leu | Asn | Pro | Ala | Ser | Leu | Gln | Cys | Glu | Leu |  |
|       |              |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |  |
| Asp   | Lys          | Asn | Asn | Ile | Pro | Thr | Arg | Ser | Tyr | Val | Ser | Tyr | Phe | Tyr | His |  |
|       |              |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |  |
| Asp   | Ser          | Leu | Tyr | Thr | Thr | Asp | Cys | Tyr | Thr | Ala | Lys | Ala | Ser | Leu | Ala |  |

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| 195                |            |           |           |            |            | 200        |           |           |            |            |            | 205       |           |           |            |  |  |
|--------------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|-----------|------------|--|--|
| Gly                | Thr<br>210 | Leu       | Ser       | Leu        | Met        | Leu<br>215 | Ile       | Cys       | Thr        | Leu        | Leu<br>220 | Glu       | Phe       | Cys       | Leu        |  |  |
| Ala<br>225         | Val        | Leu       | Thr       | Ala        | Val<br>230 | Leu        | Arg       | Trp       | Lys        | Gln<br>235 | Ala        | Tyr       | Ser       | Asp       | Phe<br>240 |  |  |
| Pro                | Gly        | Val       | Ser       | Val<br>245 | Leu        | Ala        | Gly       | Phe       | Thr<br>250 |            |            |           |           |           |            |  |  |
| <210> 127          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <400> 127          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| 000                |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <210> 128          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <211> 61           |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <212> PRT          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <213> homo sapiens |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <400> 128          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| Met<br>1           | His        | Thr       | Cys       | Gln<br>5   | Ile        | Tyr        | Ile       | Tyr       | Ser<br>10  | Thr        | Asn        | Val       | Thr       | Phe<br>15 | Leu        |  |  |
| Phe                | Phe        | Val       | Leu<br>20 | Asp        | Val        | Arg        | Ala       | Cys<br>25 | Ser        | Tyr        | Val        | Arg       | Tyr<br>30 | Leu       | His        |  |  |
| Lys                | Leu        | Leu<br>35 | His       | Tyr        | Phe        | Phe        | Leu<br>40 | Cys       | Asn        | Thr        | Phe        | Leu<br>45 | Phe       | Val       | Tyr        |  |  |
| Val                | Val<br>50  | Gln       | Ile       | Tyr        | Ser        | Phe<br>55  | Leu       | Lys       | Leu        | Leu        | Lys<br>60  | Lys       |           |           |            |  |  |
| <210> 129          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <211> 211          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <212> PRT          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <213> homo sapiens |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| <400> 129          |            |           |           |            |            |            |           |           |            |            |            |           |           |           |            |  |  |
| Pro<br>1           | Ala        | Ser       | Asn       | Arg<br>5   | Pro        | Lys        | Ser       | Gly       | Arg<br>10  | Ala        | Pro        | Glu       | Pro       | Arg<br>15 | Glu        |  |  |
| Pro                | Ala        | Arg       | Arg<br>20 | Ser        | Ala        | Gly        | Gly       | Ser<br>25 | Pro        | Pro        | Pro        | Pro       | Pro<br>30 | Trp       | Pro        |  |  |
| Arg                | Val        | Pro<br>35 | Ala       | Ala        | Ala        | Ala        | Gly<br>40 | Thr       | Glu        | Gly        | Ala        | Ser<br>45 | Pro       | Asp       | Leu        |  |  |
| Ala                | Pro<br>50  | Leu       | Arg       | Pro        | Ala        | Ala<br>55  | Pro       | Gly       | Gln        | Thr        | Pro<br>60  | Leu       | Arg       | Lys       | Glu        |  |  |
| Val<br>65          | Leu        | Lys       | Ser       | Lys        | Met<br>70  | Gly        | Lys       | Ser       | Glu        | Lys<br>75  | Ile        | Ala       | Leu       | Pro       | His<br>80  |  |  |

|            |            |            |            |            |            |            |                   |            |            |            |            |            |            |            |            |  |
|------------|------------|------------|------------|------------|------------|------------|-------------------|------------|------------|------------|------------|------------|------------|------------|------------|--|
| Gly        | Gln        | Leu        | Val        | His<br>85  | Gly        | Ile        | His <sup>66</sup> | Leu        | Tyr<br>90  | Glu        | Gln        | Pro        | Lys        | Ile<br>95  | Asn        |  |
| Arg        | Gln        | Lys        | Ser<br>100 | Lys        | Tyr        | Asn        | Leu               | Pro<br>105 | Leu        | Thr        | Lys        | Ile        | Thr<br>110 | Ser        | Ala        |  |
| Lys        | Arg        | Asn<br>115 | Glu        | Asn        | Asn        | Phe        | Trp<br>120        | Gln        | Asp        | Ser        | Val        | Ser<br>125 | Ser        | Asp        | Arg        |  |
| Ile        | Gln<br>130 | Lys        | Gln        | Glu        | Lys        | Lys<br>135 | Pro               | Phe        | Lys        | Asn        | Thr<br>140 | Glu        | Asn        | Ile        | Lys        |  |
| Asn<br>145 | Ser        | His        | Leu        | Lys        | Lys<br>150 | Ser        | Ala               | Phe        | Leu        | Thr<br>155 | Glu        | Val        | Ser        | Gln        | Lys<br>160 |  |
| Glu        | Asn        | Tyr        | Ala        | Gly<br>165 | Ala        | Lys        | Phe               | Ser        | Asp<br>170 | Pro        | Pro        | Ser        | Pro        | Ser<br>175 | Val        |  |
| Leu        | Pro        | Lys        | Pro<br>180 | Pro        | Ser        | His        | Trp               | Met<br>185 | Gly        | Ser        | Thr        | Val        | Glu<br>190 | Asn        | Ser        |  |
| Asn        | Gln        | Asn<br>195 | Arg        | Glu        | Leu        | Met        | Ala<br>200        | Val        | His        | Leu        | Lys        | Thr<br>205 | Leu        | Leu        | Lys        |  |
| Val        | Gln<br>210 | Thr        |            |            |            |            |                   |            |            |            |            |            |            |            |            |  |

<210> 130  
<400> 130  
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<210> 131  
<211> 48  
<212> PRT  
<213> homo sapiens

<400> 131

|          |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |  |
|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|--|
| Met<br>1 | Ile | Leu       | Thr       | Asn<br>5 | Pro | Leu | Lys       | Ser       | Lys<br>10 | Thr | Asp | Thr       | Phe       | Ile<br>15 | Asn |  |
| Arg      | Ser | Ile       | Cys<br>20 | Lys      | Gln | Ser | Gln       | Tyr<br>25 | Ala       | Leu | Gly | Arg       | Leu<br>30 | Thr       | Ile |  |
| Phe      | Leu | Thr<br>35 | Cys       | Gln      | Gly | Val | Leu<br>40 | Pro       | Ser       | Gln | Gln | Thr<br>45 | Pro       | Leu       | Ile |  |

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<212> PRT  
<213> homo sapiens

<400> 132

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Leu | Gly | Ile | Phe | Leu | His | Gln | Tyr | Val | Ile | Phe | Asn | Gln | Asn | Val | Lys |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|

000260"6954960



| Table 1. Demographic characteristics of the study population |             |
|--------------------------------------------------------------|-------------|
| Age (years)                                                  | 65.0 ± 1.5  |
| Gender                                                       |             |
| Male                                                         | 100         |
| Female                                                       | 100         |
| Education (years)                                            | 12.0 ± 1.0  |
| Marital status                                               |             |
| Married                                                      | 100         |
| Widowed                                                      | 100         |
| Divorced                                                     | 100         |
| Single                                                       | 100         |
| Occupation                                                   |             |
| Retired                                                      | 100         |
| Unemployed                                                   | 100         |
| Employed                                                     | 100         |
| Income (USD/month)                                           | 1,000 ± 200 |
| Health insurance                                             |             |
| Yes                                                          | 100         |
| No                                                           | 100         |
| Comorbidities                                                |             |
| Hypertension                                                 | 50          |
| Diabetes                                                     | 30          |
| Cholesterol                                                  | 20          |
| Arthritis                                                    | 10          |
| Depression                                                   | 10          |
| Medication                                                   |             |
| Antihypertensive                                             | 50          |
| Antidiabetic                                                 | 30          |
| Lipid-lowering                                               | 20          |
| Painkillers                                                  | 10          |
| Antidepressants                                              | 10          |
| Other                                                        | 10          |
| Smoking status                                               |             |
| Current                                                      | 10          |
| Former                                                       | 40          |
| Never                                                        | 50          |
| Alcohol consumption                                          |             |
| Regular                                                      | 10          |
| Occasional                                                   | 40          |
| Never                                                        | 50          |
| Family history                                               |             |
| Heart disease                                                | 20          |
| Stroke                                                       | 10          |
| Diabetes                                                     | 10          |
| Hypertension                                                 | 10          |
| Other                                                        | 10          |

<400> 133

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<210> 134
<400> 134
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<400> 135

|          |     |           |           |          |     |     |           |           |           |     |     |           |           |           |     |
|----------|-----|-----------|-----------|----------|-----|-----|-----------|-----------|-----------|-----|-----|-----------|-----------|-----------|-----|
| Leu<br>1 | Asn | Val       | Phe       | Ser<br>5 | Ser | Leu | Gln       | Ile       | Ser<br>10 | Glu | Leu | Ile       | Phe       | Pro<br>15 | Pro |
| Leu      | Pro | Met       | Trp<br>20 | His      | Pro | Leu | Pro       | Arg<br>25 | Lys       | Lys | Pro | Gly       | Met<br>30 | Tyr       | Arg |
| Gly      | Asn | Gly<br>35 | His       | Gln      | Asn | His | Tyr<br>40 | Pro       | Pro       | Pro | Val | Pro<br>45 | Phe       | Gly       | Tyr |
| Pro      | Asn | Gln       | Gly       | Arg      | Lys | Asn | Lys       | Pro       | Tyr       | Arg | Pro | Ile       | Pro       | Val       | Thr |

000260"6954960

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 68
 50 55 60

Trp Val Pro Pro Pro Gly Met His Cys Asp Arg Asn His Trp Ile Asn
 65 70 75 80

Pro His Met Leu Ala Pro His
 85

<210> 136
<400> 136
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<210> 137
<211> 83
<212> PRT
<213> homo sapiens

<400> 137

Met Tyr Gly Asn Ile Leu Cys Pro Thr Leu His Thr Pro Cys Thr Gln
 1 5 10 15

Ile Leu Tyr Cys Met Asn Tyr Ala Leu Ser Arg Ile Gln Cys Gln Gly
 20 25 30

Glu Leu Gly Glu Ile Asn Tyr Phe Asn Phe Phe Phe Ile Leu Tyr Lys
 35 40 45

Ala Met Asp Phe Ile Trp Leu Met Cys Ala Leu Tyr Thr Ser His Phe
 50 55 60

Asn Arg Met Glu Leu Leu Ile Ile Phe Gln Arg Val Ile Asp Met Gln
 65 70 75 80

Lys Phe Gln

<210> 138
<211> 366
<212> PRT
<213> homo sapiens

<400> 138

Arg Pro Lys Pro Gly His Pro Leu Tyr Ser Lys Tyr Met Arg Gly Asp
 1 5 10 15

Val Leu Val Met Leu Lys Gln Thr Glu Asn Asn Tyr Leu Glu Cys Gln
 20 25 30

Lys Gly Glu Asp Thr Gly Arg Val His Leu Ser Gln Met Lys Ile Ile
 35 40 45

Thr Pro Leu Asp Glu His Leu Arg Ser Arg Pro Asn Asp Pro Ser His
 50 55 60

Ala Gln Lys Pro Val Asp Ser Gly Ala Pro His Ala Val Val Leu His

```

000260 092000 0546559

| 65         |            |            |            | 70         |            |            |            | 69         |            |            |            | 75         |            |            |            | 80 |  |  |  |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|----|--|--|--|
| Asp        | Phe        | Pro        | Ala        | Glu<br>85  | Gln        | Val        | Asp        | Asp        | Leu<br>90  | Asn        | Leu        | Thr        | Ser        | Gly<br>95  | Glu        |    |  |  |  |
| Ile        | Val        | Tyr        | Leu<br>100 | Leu        | Glu        | Lys        | Ile        | Asp<br>105 | Thr        | Asp        | Trp        | Tyr        | Arg<br>110 | Gly        | Asn        |    |  |  |  |
| Cys        | Arg        | Asn<br>115 | Gln        | Ile        | Gly        | Ile        | Phe<br>120 | Pro        | Ala        | Asn        | Tyr        | Val<br>125 | Lys        | Val        | Ile        |    |  |  |  |
| Ile        | Asp<br>130 | Ile        | Pro        | Glu        | Gly        | Gly<br>135 | Asn        | Gly        | Lys        | Arg        | Glu<br>140 | Cys        | Val        | Ser        | Ser        |    |  |  |  |
| His<br>145 | Cys        | Val        | Lys        | Gly        | Ser<br>150 | Arg        | Cys        | Val        | Ala        | Arg<br>155 | Phe        | Glu        | Tyr        | Ile        | Gly<br>160 |    |  |  |  |
| Glu        | Gln        | Lys        | Asp        | Glu<br>165 | Leu        | Ser        | Phe        | Ser        | Glu<br>170 | Gly        | Glu        | Ile        | Ile        | Ile<br>175 | Leu        |    |  |  |  |
| Lys        | Glu        | Tyr        | Val<br>180 | Asn        | Glu        | Glu        | Trp        | Ala<br>185 | Arg        | Gly        | Glu        | Val        | Arg<br>190 | Gly        | Arg        |    |  |  |  |
| Thr        | Gly        | Ile<br>195 | Phe        | Pro        | Leu        | Asn        | Phe<br>200 | Val        | Glu        | Pro        | Val        | Glu<br>205 | Asp        | Tyr        | Pro        |    |  |  |  |
| Thr        | Ser<br>210 | Gly        | Ala        | Asn        | Val        | Leu<br>215 | Ser        | Thr        | Lys        | Val        | Pro<br>220 | Leu        | Lys        | Thr        | Lys        |    |  |  |  |
| Lys<br>225 | Glu        | Asp        | Ser        | Gly        | Ser<br>230 | Asn        | Ser        | Gln        | Val        | Asn<br>235 | Ser        | Leu        | Pro        | Ala        | Glu<br>240 |    |  |  |  |
| Trp        | Cys        | Glu        | Ala        | Leu<br>245 | His        | Ser        | Phe        | Thr        | Ala<br>250 | Glu        | Thr        | Ser        | Asp        | Asp<br>255 | Leu        |    |  |  |  |
| Ser        | Phe        | Lys        | Arg<br>260 | Gly        | Asp        | Arg        | Ile        | Gln<br>265 | Ile        | Leu        | Glu        | Arg        | Leu<br>270 | Asp        | Ser        |    |  |  |  |
| Asp        | Trp        | Cys<br>275 | Arg        | Gly        | Arg        | Leu        | Gln<br>280 | Asp        | Arg        | Glu        | Gly        | Ile<br>285 | Phe        | Pro        | Ala        |    |  |  |  |
| Val        | Phe<br>290 | Val        | Arg        | Pro        | Cys        | Pro<br>295 | Ala        | Glu        | Ala        | Lys        | Ser<br>300 | Met        | Leu        | Ala        | Ile        |    |  |  |  |
| Val<br>305 | Pro        | Lys        | Gly        | Arg        | Lys<br>310 | Ala        | Lys        | Ala        | Leu        | Tyr<br>315 | Asp        | Phe        | Arg        | Gly        | Glu<br>320 |    |  |  |  |
| Asn        | Glu        | Asp        | Glu        | Leu<br>325 | Ser        | Phe        | Lys        | Ala        | Gly<br>330 | Asp        | Ile        | Ile        | Thr        | Glu<br>335 | Leu        |    |  |  |  |

Glu Ser Val Asp Asp Asp Trp Met Ser Gly Glu Leu Met Gly Lys Ser  
340 345 350

Gly Ile Phe Pro Lys Asn Tyr Ile Gln Phe Leu Gln Ile Ser  
355 360 365

<210> 139  
<211> 68  
<212> PRT  
<213> homo sapiens

<400> 139

Met Asn Pro Tyr Ile Ser Ile Ile Val Phe Ile Val Phe Leu Cys Ser  
1 5 10 15

Glu Asn Tyr Pro Trp Asn Asn Met Leu Arg Ile Thr Gly Ser Ser Pro  
20 25 30

Tyr Leu His Phe Leu Ser Val Leu Gly Val Leu Val Asn Ser Tyr Val  
35 40 45

Leu Ile Leu Phe Asn Ser Glu Phe Leu Thr Gln His Phe Arg Glu Arg  
50 55 60

Ile Gln Ala Gly  
65

<210> 140  
<211> 28  
<212> PRT  
<213> homo sapiens

<400> 140

Phe Phe Phe Phe Phe Phe Leu Leu Leu Lys Phe Phe Phe Asn Lys Asp  
1 5 10 15

Lys Gly Phe Asn Asn Phe Cys Ala Thr Ile Leu Asn  
20 25

<210> 141  
<211> 22  
<212> PRT  
<213> homo sapiens

<400> 141

Glu Gly Thr Thr Arg Lys Lys Asp Lys Tyr Ile Leu Ser Leu Glu Asn  
1 5 10 15

Ala Ser Arg Gln Lys Tyr  
20

<210> 142  
<211> 46  
<212> PRT  
<213> homo sapiens

000260" 69594960

&lt;400&gt; 142

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Phe | Leu | Arg | Lys | Phe | Asp | Arg | Leu | Val | Arg | Thr | Ser | Asp | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Ile | Ser | Leu | Lys | Trp | Val | Ser | Trp | Asn | Phe | Ile | Phe | Asp | Asn | Ile |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Tyr | Thr | Ile | Pro | Asn | Ser | Phe | Ala | Val | Leu | Arg | Phe | Val | Gly |     |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

&lt;210&gt; 143

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 143

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Gly | Trp | Gly | Met | Ser | Ser | Ile | Asn | Pro | Tyr | Gly | Met | His | Ser |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gln | Trp | Pro | Ser | His | Leu | Gly | Leu | Glu | Pro | Leu | Val | Gln | Gly | Leu | Gly |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Glu | Asn | Arg | Pro | His | Gly | Asn | Ser | His | Thr | Val | Ile | Ala | Phe | Asn | Thr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Glu | Pro | Arg | Val | Pro | Lys | Gln | Gln |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 144

&lt;211&gt; 56

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 144

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asn | Ile | Ser | Thr | Gln | Gly | Arg | Ala | Lys | Gly | Val | Pro | Arg | Ile | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ala | Lys | Gly | Gln | Val | Leu | Ile | Glu | Gly | Leu | Glu | Leu | Ser | Arg | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Met | Glu | Ala | Ala | Cys | Thr | Leu | Gly | Ala | Cys | Pro | Asp | Ser | Ser | Leu | Gly |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Pro | Phe | Tyr | Leu | Ser | Ser | Phe |     |     |     |     |     |     |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     |     |     |     |     |     |

&lt;210&gt; 145

&lt;211&gt; 109

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 145

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Pro | Lys | Gly | Lys | Ala | Phe | Arg | Arg | Thr | Leu | Arg | Ile | Thr | Ser | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

000250" 59594360

|           |           |           |            |           |           |           |                   |            |           |           |           |           |           |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-------------------|------------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Phe       | Phe       | Ser       | Ser<br>20  | Leu       | Leu       | Leu       | Leu <sup>72</sup> | Gln<br>25  | Leu       | Leu       | Phe       | Gly       | His<br>30 | His       | Leu       |
| Leu       | Val       | Leu<br>35 | Val        | Ser       | Pro       | Gln       | Leu<br>40         | Pro        | Gly       | Ala       | Val       | Phe<br>45 | Glu       | Gly       | Glu       |
| Ala       | Phe<br>50 | Ser       | Val        | Pro       | Pro       | Pro<br>55 | Gln               | Ala        | Leu       | Pro       | Met<br>60 | Met       | Ala       | Pro       | Ser       |
| His<br>65 | His       | Pro       | Ser        | Pro       | Ala<br>70 | Pro       | Leu               | Pro        | Ala       | Ser<br>75 | Pro       | Pro       | Pro       | Pro       | Ala<br>80 |
| Pro       | Pro       | Pro       | Pro        | Trp<br>85 | Arg       | Arg       | Arg               | Gly        | Ile<br>90 | Pro       | Leu       | Ala       | Phe       | Gly<br>95 | Leu       |
| Pro       | Arg       | Ser       | Arg<br>100 | Arg       | Leu       | Pro       | Glu               | Leu<br>105 | Pro       | Gln       | Pro       | Arg       |           |           |           |

<210> 146  
 <211> 247  
 <212> PRT  
 <213> homo sapiens  
 <400> 146

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Arg<br>1  | Pro        | Ala        | Pro        | Ala<br>5  | Pro       | Arg        | Cys        | Gln        | Leu<br>10 | Pro       | Gln        | Arg        | Pro        | Ala<br>15 | Glu       |
| Ala       | Arg        | Cys        | Met<br>20  | Leu       | Ser       | Arg        | Cys        | Arg<br>25  | Ser       | Arg       | Leu        | Leu        | His<br>30  | Val       | Leu       |
| Gly       | Leu        | Ser<br>35  | Phe        | Leu       | Leu       | Gln        | Thr<br>40  | Arg        | Arg       | Pro       | Ile        | Leu<br>45  | Leu        | Cys       | Ser       |
| Pro       | Arg<br>50  | Leu        | Met        | Lys       | Pro       | Leu<br>55  | Val        | Val        | Phe       | Val       | Leu<br>60  | Gly        | Gly        | Pro       | Gly       |
| Ala<br>65 | Gly        | Lys        | Gly        | Thr       | Gln<br>70 | Cys        | Ala        | Arg        | Ile       | Val<br>75 | Glu        | Lys        | Tyr        | Gly       | Tyr<br>80 |
| Thr       | His        | Leu        | Ser        | Ala<br>85 | Gly       | Glu        | Leu        | Leu        | Arg<br>90 | Asp       | Glu        | Arg        | Lys        | Asn<br>95 | Pro       |
| Asp       | Ser        | Gln        | Tyr<br>100 | Gly       | Glu       | Leu        | Ile        | Glu<br>105 | Lys       | Tyr       | Ile        | Lys        | Glu<br>110 | Gly       | Lys       |
| Ile       | Val        | Pro<br>115 | Val        | Glu       | Ile       | Thr        | Ile<br>120 | Ser        | Leu       | Leu       | Lys        | Arg<br>125 | Glu        | Met       | Asp       |
| Gln       | Thr<br>130 | Met        | Ala        | Ala       | Asn       | Ala<br>135 | Gln        | Lys        | Asn       | Lys       | Phe<br>140 | Leu        | Ile        | Asp       | Gly       |

000260-69594950



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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ala | Leu | Val | Gln | Lys | His | Leu | Thr | Lys | Leu | Arg | His | Trp | Gln | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Leu | Glu | Asp | Ile | Asn | Val | Gln | His | Lys | Lys | Pro | Ala | Asp | Ile | Pro |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Gln | Gly | Ser | Leu | Ala | Tyr | Leu | Glu | Gln | Ala | Ser | Ala | Asn | Ile | Pro | Ala |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Pro | Leu | Lys | Pro | Thr |     |     |     |     |     |     |     |     |     |     |     |
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<400> 148

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| Met | Leu | Arg | Asp | Leu | Gln | Leu | Gln | Ile | Leu | Arg | Asn | Val | Thr | His | His |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Ser | Val | Thr | Lys | Gln | Leu | Pro | Thr | Ser | Glu | Ala | Val | Val | Ser | Ala |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Ser | Glu | Ala | Gly | Ala | Ser | Gly | Ile | Thr | Glu | Ala | Gln | Ala | Arg | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ile | Val | Asn | Ser | Ala | Leu | Lys | Leu | Tyr | Ser | Gln | Asp | Lys | Thr | Gly | Met |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Asp | Phe | Ala | Leu | Glu | Ser | Gly | Gly | Gly | Ser | Ile | Leu | Ser | Thr | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Cys | Ser | Glu | Thr | Tyr | Glu | Thr | Lys | Thr | Ala | Leu | Met | Ser | Leu | Phe | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Ile | Pro | Leu | Trp | Tyr | Phe | Ser | Gln | Ser | Pro | Arg | Val | Val | Ile | Gln | Pro |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Asp | Ile | Tyr | Pro | Gly | Asn | Cys | Trp | Ala | Phe | Lys | Gly | Ser | Gln | Gly | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Leu | Val | Val | Arg | Leu | Ser | Met | Met | Ile | His | Pro | Ala | Ala | Phe | Thr | Leu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | His | Ile | Pro | Lys | Thr | Leu | Ser | Pro | Thr | Gly | Asn | Ile | Ser | Ser | Ala |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Pro | Lys | Asp | Phe | Ala | Val | Tyr | Gly | Leu | Glu | Asn | Glu | Tyr | Gln | Glu | Glu |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |

000250-5954960





000260" 69944560

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| Glu        | Gln        | Arg        | Pro<br>20  | Pro        | Ala        | Gly        | Pro        | Ala<br>25  | Ser        | Ala        | Trp        | Ser        | Ser<br>30  | Ser        | Tyr        |
| Pro        | His        | Ala<br>35  | Pro        | Tyr        | Leu        | Gly        | Ser<br>40  | Ala        | Arg        | Ser        | Leu        | Ser<br>45  | Pro        | His        | Lys        |
| Met        | Ala<br>50  | Asp        | Gly        | Gly        | Ser        | Pro<br>55  | Phe        | Leu        | Gly        | Arg        | Arg<br>60  | Asp        | Phe        | Val        | Tyr        |
| Pro<br>65  | Ser        | Ser        | Thr        | Arg        | Asp<br>70  | Pro        | Ser        | Ala        | Ser        | Asn<br>75  | Gly        | Gly        | Gly        | Ser        | Pro<br>80  |
| Ala        | Arg        | Arg        | Glu        | Glu<br>85  | Lys        | Lys        | Arg        | Lys        | Ala<br>90  | Ala        | Arg        | Leu        | Lys        | Phe<br>95  | Asp        |
| Phe        | Gln        | Ala        | Gln<br>100 | Ser        | Pro        | Lys        | Glu        | Leu<br>105 | Thr        | Leu        | Gln        | Lys        | Gly<br>110 | Asp        | Ile        |
| Val        | Tyr        | Ile<br>115 | His        | Lys        | Glu        | Val        | Asp<br>120 | Lys        | Asn        | Trp        | Leu        | Glu<br>125 | Gly        | Glu        | His        |
| His        | Gly<br>130 | Arg        | Leu        | Gly        | Ile        | Phe<br>135 | Pro        | Ala        | Asn        | Tyr        | Val<br>140 | Glu        | Val        | Leu        | Pro        |
| Ala<br>145 | Asp        | Glu        | Ile        | Pro        | Lys<br>150 | Pro        | Ile        | Lys        | Pro        | Pro<br>155 | Thr        | Tyr        | Gln        | Val        | Leu<br>160 |
| Glu        | Tyr        | Gly        | Glu        | Ala<br>165 | Val        | Ala        | Gln        | Tyr        | Thr<br>170 | Phe        | Lys        | Gly        | Asp        | Leu<br>175 | Glu        |
| Val        | Glu        | Leu        | Ser<br>180 | Phe        | Arg        | Lys        | Gly        | Glu<br>185 | His        | Ile        | Cys        | Leu        | Ile<br>190 | Arg        | Lys        |
| Val        | Asn        | Glu<br>195 | Asn        | Trp        | Tyr        | Glu        | Gly<br>200 | Arg        | Ile        | Thr        | Gly        | Thr<br>205 | Gly        | Arg        | Gln        |
| Gly        | Ile<br>210 | Phe        | Pro        | Ala        | Ser        | Tyr<br>215 | Val        | Gln        | Val        | Ser        | Arg<br>220 | Glu        | Pro        | Arg        | Leu        |
| Arg<br>225 | Leu        | Cys        | Asp        | Asp        | Gly<br>230 | Pro        | Gln        | Leu        | Pro        | Thr<br>235 | Ser        | Pro        | Arg        | Leu        | Thr<br>240 |
| Ala        | Ala        | Ala        | Arg        | Ser<br>245 | Ala        | Arg        | Asp        | Pro        | Ser<br>250 | Ala        | Pro        | Ser        | Ala        | Leu<br>255 | Arg        |
| Ser        | Pro        | Ala        | Asp<br>260 | Pro        | Thr        | Asp        | Leu        | Gly<br>265 | Gly        | Gln        | Thr        | Ser        | Pro<br>270 | Arg        | Arg        |

Thr Gly Phe Ser Phe Pro Thr Gln Glu Pro Arg Pro Gln Thr Gln Asn  
275 280 285

Leu Gly Thr Pro Gly Pro Ala Leu Ser His Ser Arg Gly Pro Ser His  
290 295 300

Pro Leu Asp Leu Gly Thr Ser Ser Pro Asn Thr Ser Gln Ile His Trp  
305 310 315 320

Thr Pro Tyr Arg Ala Met Tyr Gln Tyr Arg Pro Gln Asn Glu Asp Glu  
325 330 335

Leu Glu Leu Arg Glu Gly Asp Arg Val Asp Val Met Gln Gln Cys Asp  
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Phe Pro Gly Asn Tyr Val Ala Pro Val  
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<212> PRT

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<400> 154

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| Gly<br>1  | Thr       | Pro       | Gly       | Pro<br>5  | Tyr       | Pro       | Gly       | Pro       | Leu<br>10 | Ser       | Pro       | Pro       | Pro       | Glu<br>15 | Ala       |
| Pro       | Pro       | Leu       | Glu<br>20 | Ser       | Ala       | Glu       | Pro       | Leu<br>25 | Gly       | Pro       | Ala       | Ala       | Asp<br>30 | Leu       | Trp       |
| Ala       | Asp       | Val<br>35 | Asp       | Leu       | Thr       | Glu       | Phe<br>40 | Asp       | Gln       | Tyr       | Leu       | Asn<br>45 | Cys       | Ser       | Arg       |
| Thr       | Arg<br>50 | Pro       | Asp       | Ala       | Pro       | Gly<br>55 | Leu       | Pro       | Tyr       | His       | Val<br>60 | Ala       | Leu       | Ala       | Lys       |
| Leu<br>65 | Gly       | Pro       | Arg       | Ala       | Met<br>70 | Ser       | Cys       | Pro       | Glu       | Glu<br>75 | Ser       | Ser       | Leu       | Ile       | Ser<br>80 |
| Ala       | Leu       | Ser       | Asp       | Ala<br>85 | Ser       | Ser       | Ala       | Val       | Tyr<br>90 | Tyr       | Ser       | Ala       | Cys       | Ile<br>95 | Ser       |

Gly

&lt;210&gt; 158

&lt;211&gt; 173

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 158

|           |           |            |            |           |           |           |            |            |           |           |           |            |            |           |           |
|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|-----------|------------|------------|-----------|-----------|
| Gly<br>1  | Leu       | Phe        | Pro        | Ala<br>5  | Val       | Cys       | Pro        | Trp        | Pro<br>10 | Ala       | Leu       | Asp        | Leu        | Leu<br>15 | Ser       |
| Gly       | Pro       | Gln        | Trp<br>20  | Gln       | Arg       | Gly       | Pro        | Gly<br>25  | Pro       | Gly       | Ala       | Gly        | Val<br>30  | Gly       | Asp       |
| Pro       | Gly       | Leu<br>35  | Ser        | Ala       | Val       | Ala       | Phe<br>40  | Trp        | Trp       | Gly       | Ala       | Met<br>45  | Glu        | Thr       | Gly       |
| Asn       | Gln<br>50 | Ala        | Val        | Gly       | Ser       | Gln<br>55 | Arg        | Trp        | Ser       | Leu       | Arg<br>60 | Gly        | Glu        | Trp       | Arg       |
| Ala<br>65 | Phe       | Cys        | Phe        | Cys       | Leu<br>70 | Val       | Pro        | Pro        | His       | Gly<br>75 | Thr       | Trp        | Phe        | Pro       | Gly<br>80 |
| Glu       | Asn       | Glu        | Arg        | Arg<br>85 | Gly       | Glu       | Val        | Glu        | Asn<br>90 | Arg       | Thr       | Phe        | His        | Lys<br>95 | Gly       |
| Tyr       | Phe       | Leu        | Ile<br>100 | Gly       | Cys       | Lys       | Met        | Leu<br>105 | Met       | Pro       | Arg       | Met        | Met<br>110 | Ile       | Phe       |
| Phe       | Pro       | Ala<br>115 | Asp        | Glu       | Thr       | Ile       | Arg<br>120 | Lys        | Gly       | Leu       | Arg       | Leu<br>125 | Trp        | Gln       | Val       |

000260"69594960



|            |            |            |            |           |            |            |            |            |           |           |            |            |            |           |           |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Ser<br>65  | Ser        | Glu        | Trp        | Leu       | His<br>70  | Ala        | Ala        | Ala        | Ala       | Cys<br>75 | Val        | His        | Leu        | Pro       | Ser<br>80 |
| Thr        | Gln        | Asp        | Ser        | Pro<br>85 | Arg        | Gln        | Gln        | Leu        | Val<br>90 | Phe       | Thr        | Cys        | Pro        | Pro<br>95 | Pro       |
| Arg        | Thr        | Val        | Pro<br>100 | Gly       | Leu        | Ala        | Pro        | Gly<br>105 | Cys       | Arg       | Gly        | Ser        | Ala<br>110 | Glu       | Gly       |
| Ala        | Ser        | Cys<br>115 | Pro        | Ile       | Ser        | Leu        | Ala<br>120 | Asn        | Ser       | Leu       | Leu        | Leu<br>125 | Leu        | Gly       | Pro       |
| His        | Lys<br>130 | Arg        | His        | Gly       | Arg        | Met<br>135 | Phe        | Leu        | Ile       | Arg       | Gln<br>140 | Glu        | His        | Arg       | Thr       |
| Pro<br>145 | Asn        | Pro        | Ser        | Leu       | Cys<br>150 | Leu        | Ala        |            |           |           |            |            |            |           |           |

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3096



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| gatttttacca | gcttgacttt  | tactgtctcag | atgctttctt | tccccccctt | agacgtgtta | 180 |
| attctcttgg  | gaagatgtaac | tattctttaag | gttttttcag | ataccacctt | tagttgttaa | 240 |
| ttggaatggt  | taattttctc  | qgaactttta  | aatqaaaaat | tqgaatqgta | agttacaaaa | 300 |

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| gggcqatttcc | agcaactgcc | acggactgct | gggtcagttc | ctgaatacgg | atgccagact | 600 |
| ccacaaagac  | ccctcagggc | caggacagaa | cctcactcac | cctctgctcc | ttcaggtggg | 660 |





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<210> 172  
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<400> 172

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<213> homo sapiens

<400> 173
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<211> 1679
<212> DNA
<213> homo sapiens

<400> 174
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| ttagaaaaact | gaagcttcaa | gaacagactt | gcctaacaac | aggaaaacttg | tatgtctcga | 120 |
| agtggcaatt  | cacacataag | gtccactgac | tcttgaacgc | ctcacaaata  | ttagttggct | 180 |
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| gagttaaaac  | ctctttggag | ctcttgagga | ctcagctgga | accaacgggc  | acagttggca | 420 |
| acaccatcat  | gacatcacaa | cctgttccca | atgagaccat | catatgctgc  | ccatcaaatg | 480 |
| tcatcaactt  | ctoccaagca | gagaaacccg | aaccaccaa  | ccaggggcag  | gatagcctga | 540 |
| agaaaactct  | acacgcagaa | atcaaaagta | ttgggactat | ccagatcttg  | tgtggcatga | 600 |
| tggtattgag  | cttggggatc | attttggcat | ctgtctcctt | ctctccaaat  | tttacccaag | 660 |
| tgacttctac  | actgttgaac | tctgtctaac | cattcatagg | accctttttt  | tttatcatct | 720 |
| ctggctctct  | atcaatcgcc | acagagaaaa | ggttaaccaa | gcttttggtg  | catagctgcc | 780 |
| tggttggaag  | cattctgagt | gctctgtctg | ccttggtggg | tttcattatc  | ctgtcagctc | 840 |
| aacagccac   | cttaaatcct | gcctcactgc | agtgtgaatt | qqacaaaaat  | aatatacca  | 900 |



```

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```

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<210> 175
<211> 2411
<212> DNA
<213> homo sapiens

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<400> 175
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<210> 176  
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<400> 176

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3450

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 <211> 874  
 <212> DNA  
 <213> homo sapiens

<400> 177

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| ggccccggct | ctattctggg | ctgcgggect | gggaagggtc  | cgccgggtgc  | caaatgagct  | 120 |
| gtcctaactc | tgcggggctg | cagcttcctg | catgatgctg  | gggagcttgg  | cgcccgaccc  | 180 |
| aggatctaga | aggcactctg | ggcaggccgc | gctccgcccc  | cgaagggtacc | caaccctctg  | 240 |
| ggatagatgc | aggaagcgat | ggttaagacc | catttttcacc | caacttctcg  | ccgcagctctg | 300 |
| gcttaccaca | cgctcctccc | cattcccagt | gagccgcttt  | ttgcagcacc  | aggcgaacac  | 360 |
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| tgatcacaca | gattcctact | tgggctcttt | cctttaatct  | tcggaggctg  | agtttgccca  | 480 |
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| ttctcttcac | cttatcaaaa | cctgagctaa | aaccaatgca  | tcagctgatg  | atgacagcag  | 600 |
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| ttatggtaat | ctggaattgt | attttgtaat | attaagtgtt  | ttgaacctct  | aacattttacc | 840 |
| ttccccaaaa | atcgaaacct | caggtttcaa | aaat        |             |             | 874 |

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 <213> homo sapiens

<400> 178

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| atccggcact  | gcaacaatgg | aatccctgag  | gactccaagg | tagagggccc | tgcgttcaca  | 120  |
| gatgccatcc  | gcatgtaccg | acagtccaag  | gagctgtacg | gcacctggga | gatgctgtgt  | 180  |
| gggaacgagg  | tgcatatcct | gagcaacctg  | gtgatggagg | agctgggccc | tgagctgaag  | 240  |
| gcagagctcg  | gcccgcggtc | gaaggggaaa  | ccgcaggagc | ggcagcggca | gtggatccag  | 300  |
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| ctgtccaagg  | tgacgcaggt | gcagccggcc  | atgcaggccg | tcatccgaac | tgacatggac  | 420  |
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| aagetgtccc  | gcttggcgta | ccaccccttg  | aagatgcaga | gctgctatga | gaagatggag  | 720  |
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| ctcctgcacc  | aggagctggg | gaagggggccc | accaaggagg | agctgtgcaa | gtccatccag  | 900  |
| cggttccttg  | agcgggtgct | gaagaaatcc  | gactacgaca | gcagctctgt | gcggaagagg  | 960  |
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| atgcacaaca  | gcgaccccaa | cctgcacctg  | ctggccgagg | gcgcccccat | cgactggggc  | 1260 |
| gaggagtaca  | gcaacagcgg | cgggggcgcc  | agcccagccc | cagcaccctg | gagtcagcca  | 1320 |
| ccctctcgga  | aaagcgacgg | cgcgccaagc  | aggtggtctc | tgtggtccag | gatgaggagg  | 1380 |
| tggggctgcc  | cttttaggct | agccctgagt  | caccaccacc | tgcgtccccg | gacggtgtcal | 1440 |
| ctgagatccg  | aggcctgccc | gcccaggctc  | tgggcctga  | gagcccccca | ccagccggcc  | 1500 |
| ccctgctcaa  | cggggcctcc | gctggggaga  | gtccccagcc | taaggccgcc | cccaggccct  | 1560 |
| cctcgccgcc  | tgcttcaccc | ctccagcatc  | tcctgcctgg | aaaggctgtg | gaccttgggc  | 1620 |
| cccccaagcc  | cagcgaccag | gagactggag  | agcaggtgtc | cagccccagc | agccaccccg  | 1680 |
| ccctccacac  | caccacccag | gacagtgcag  | gggtgcagac | tgagttctag | gccagtgggt  | 1740 |
| ccctgactgc  | tgacacatgg | acaggccgtt  | cccttcggga | cccaggcagg | ctcagctctg  | 1800 |
| gggagggcac  | cctggtctgt | gccttctggg  | tggaggcggg | gcagggtgtg | gtggcaccgc  | 1860 |
| caggggagcgg | gccccactga | gtcactttat  | tgggttcagt | caacactttc | ttgctccctg  | 1920 |

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```

3265

&lt;210&gt; 179

&lt;211&gt; 262

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 179

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Leu | Cys | Val | Phe | Pro | Ser | Ser | Ala | Ala | Ser | Phe | Leu | Ser | Phe | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Ala | Leu | Val | Val | Ala | Ala | Thr | Met | Asn | Lys | Lys | Lys | Lys | Pro | Phe | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Gly | Met | Pro | Ala | Pro | Leu | Gly | Tyr | Val | Pro | Gly | Leu | Gly | Arg | Gly | Ala |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Thr | Gly | Phe | Thr | Thr | Arg | Ser | Asp | Ile | Gly | Pro | Ala | Arg | Asp | Ala | Asn |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Asp | Pro | Val | Asp | Asp | Arg | His | Ala | Pro | Pro | Gly | Lys | Arg | Thr | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asp | Gln | Met | Lys | Lys | Asn | Gln | Ala | Ala | Asp | Asp | Asp | Asp | Glu | Asp | Leu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Asp | Thr | Asn | Tyr | Asp | Glu | Phe | Asn | Gly | Tyr | Ala | Gly | Ser | Leu | Phe |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | Ser | Gly | Pro | Tyr | Glu | Lys | Asp | Asp | Glu | Glu | Ala | Asp | Ala | Ile | Tyr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Ala | Ala | Leu | Asp | Lys | Arg | Met | Asp | Glu | Arg | Arg | Lys | Glu | Arg | Arg | Glu |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

000260 " 69594660

|            |     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Gln<br>145 | Arg | Glu | Lys | Glu | Glu<br>150 | Ile | Glu | Lys | Tyr | Arg<br>155 | Met | Glu | Arg | Pro | Lys<br>160 |
|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |     |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|
| Ile | Gln | Gln | Gln | Phe<br>165 | Ser | Asp | Leu | Lys | Arg<br>170 | Lys | Leu | Ala | Glu | Val<br>175 | Thr |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|

|     |     |     |            |     |     |     |     |            |     |     |     |     |            |     |     |
|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|
| Glu | Glu | Glu | Trp<br>180 | Leu | Ser | Ile | Pro | Glu<br>185 | Val | Gly | Asp | Ala | Arg<br>190 | Asn | Lys |
|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|

|     |     |            |     |     |     |     |            |     |     |     |     |            |     |     |     |
|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|
| Arg | Gln | Arg<br>195 | Asn | Pro | Arg | Tyr | Glu<br>200 | Lys | Leu | Thr | Pro | Val<br>205 | Pro | Asp | Ser |
|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|

|     |            |     |     |     |     |            |     |     |     |     |            |     |     |     |     |
|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|
| Phe | Phe<br>210 | Ala | Lys | His | Leu | Gln<br>215 | Thr | Gly | Glu | Asn | His<br>220 | Thr | Ser | Val | Asp |
|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|

|            |     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |
|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|
| Pro<br>225 | Arg | Gln | Thr | Gln | Phe<br>230 | Gly | Gly | Leu | Asn | Thr<br>235 | Pro | Tyr | Pro | Gly | Gly<br>240 |
|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|

|     |     |     |     |            |     |     |     |     |            |     |     |     |     |            |     |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|
| Leu | Asn | Thr | Pro | Tyr<br>245 | Pro | Gly | Gly | Met | Thr<br>250 | Pro | Gly | Leu | Met | Thr<br>255 | Pro |
|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|

|     |     |     |            |     |     |
|-----|-----|-----|------------|-----|-----|
| Gly | Thr | Val | Ser<br>260 | Trp | Thr |
|-----|-----|-----|------------|-----|-----|

<210> 180  
 <211> 467  
 <212> PRT  
 <213> homo sapiens

<400> 180

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| His<br>1 | Thr | Leu | Ser | Arg<br>5 | Trp | Thr | Lys | His | Ser<br>10 | Ile | Pro | Arg | Trp | Asn<br>15 | Asp |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|

|     |     |     |           |     |     |     |     |           |     |     |     |     |           |     |     |
|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|
| Ala | Arg | Thr | Asp<br>20 | Asp | Thr | Trp | His | Ser<br>25 | Glu | Leu | Asp | Met | Arg<br>30 | Lys | Ile |
|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|

|     |     |           |     |     |     |     |           |     |     |     |     |           |     |     |     |
|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|
| Gly | Gln | Ala<br>35 | Arg | Asn | Thr | Leu | Met<br>40 | Asp | Met | Arg | Leu | Ser<br>45 | Gln | Val | Ser |
|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|

|     |           |     |     |     |     |           |     |     |     |     |           |     |     |     |     |
|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|
| Asp | Ser<br>50 | Val | Ser | Gly | Gln | Thr<br>55 | Val | Val | Asp | Pro | Lys<br>60 | Gly | Tyr | Leu | Thr |
|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|

|           |     |     |     |     |           |     |     |     |     |           |     |     |     |     |           |
|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|
| Asp<br>65 | Leu | Asn | Ser | Met | Ile<br>70 | Pro | Thr | His | Gly | Gly<br>75 | Asp | Ile | Asn | Asp | Ile<br>80 |
|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|

|     |     |     |     |           |     |     |     |     |           |     |     |     |     |           |     |
|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Lys | Lys | Ala | Arg | Leu<br>85 | Leu | Leu | Lys | Ser | Val<br>90 | Arg | Glu | Thr | Asn | Pro<br>95 | His |
|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|

|     |     |     |            |     |     |     |     |            |     |     |     |     |            |     |     |
|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|
| His | Pro | Pro | Ala<br>100 | Trp | Ile | Ala | Ser | Ala<br>105 | Arg | Leu | Glu | Glu | Val<br>110 | Thr | Gly |
|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|-----|-----|------------|-----|-----|

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|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Lys        | Leu        | Gln<br>115 | Val        | Ala        | Arg        | Asn        | Leu<br>120 | Ile        | Met        | Lys        | Gly        | Thr<br>125 | Glu        | Met        | Cys        |
| Pro        | Lys<br>130 | Ser        | Glu        | Asp        | Val        | Trp<br>135 | Leu        | Glu        | Ala        | Ala        | Arg<br>140 | Leu        | Gln        | Pro        | Gly        |
| Asp<br>145 | Thr        | Ala        | Lys        | Ala        | Val<br>150 | Val        | Ala        | Gln        | Ala        | Val<br>155 | Arg        | His        | Leu        | Pro        | Gln<br>160 |
| Ser        | Val        | Arg        | Ile        | Tyr<br>165 | Ile        | Arg        | Ala        | Ala        | Glu<br>170 | Leu        | Glu        | Thr        | Asp        | Ile<br>175 | Arg        |
| Ala        | Lys        | Lys        | Arg<br>180 | Val        | Leu        | Arg        | Lys        | Ala<br>185 | Leu        | Glu        | His        | Val        | Pro<br>190 | Asn        | Ser        |
| Val        | Arg        | Leu<br>195 | Trp        | Lys        | Ala        | Ala        | Val<br>200 | Glu        | Leu        | Glu        | Glu        | Pro<br>205 | Glu        | Asp        | Ala        |
| Arg        | Ile<br>210 | Met        | Leu        | Ser        | Arg        | Ala<br>215 | Val        | Glu        | Cys        | Cys        | Pro<br>220 | Thr        | Ser        | Val        | Glu        |
| Leu<br>225 | Trp        | Leu        | Ala        | Leu        | Ala<br>230 | Arg        | Leu        | Glu        | Thr        | Tyr<br>235 | Glu        | Asn        | Ala        | Arg        | Lys<br>240 |
| Val        | Leu        | Asn        | Lys        | Ala<br>245 | Arg        | Glu        | Asn        | Ile        | Pro<br>250 | Thr        | Asp        | Arg        | His        | Ile<br>255 | Trp        |
| Ile        | Thr        | Ala        | Ala<br>260 | Lys        | Leu        | Glu        | Glu        | Ala<br>265 | Asn        | Gly        | Asn        | Thr        | Gln<br>270 | Met        | Val        |
| Glu        | Lys        | Ile<br>275 | Ile        | Asp        | Arg        | Ala        | Ile<br>280 | Thr        | Ser        | Leu        | Arg        | Ala<br>285 | Asn        | Gly        | Val        |
| Glu        | Ile<br>290 | Asn        | Arg        | Glu        | Gln        | Trp<br>295 | Ile        | Gln        | Asp        | Ala        | Glu<br>300 | Glu        | Cys        | Asp        | Arg        |
| Ala<br>305 | Gly        | Ser        | Val        | Ala        | Thr<br>310 | Cys        | Gln        | Ala        | Val        | Met<br>315 | Arg        | Ala        | Val        | Ile        | Gly<br>320 |
| Ile        | Gly        | Ile        | Glu        | Glu<br>325 | Glu        | Asp        | Arg        | Lys        | His<br>330 | Thr        | Trp        | Met        | Glu        | Asp<br>335 | Ala        |
| Asp        | Ser        | Cys        | Val<br>340 | Ala        | His        | Asn        | Ala        | Leu<br>345 | Glu        | Cys        | Ala        | Arg        | Ala<br>350 | Ile        | Tyr        |
| Ala        | Tyr        | Ala<br>355 | Leu        | Gln        | Val        | Phe        | Pro<br>360 | Ser        | Lys        | Lys        | Ser        | Val<br>365 | Trp        | Leu        | Arg        |

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Ala | Tyr | Phe | Glu | Lys | Asn | His | Gly | Thr | Arg | Glu | Ser | Leu | Glu | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Gln | Arg | Ala | Val | Ala | His | Cys | Pro | Lys | Ala | Glu | Val | Leu | Trp |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Met | Gly | Ala | Lys | Ser | Lys | Trp | Leu | Ala | Gly | Asp | Val | Pro | Ala | Ala |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Ile | Leu | Ala | Leu | Ala | Phe | Gln | Ala | Asn | Pro | Asn | Ser | Glu | Glu |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Trp | Leu | Ala | Ala | Val | Lys | Leu | Glu | Ser | Glu | Asn | Asp | Glu | Tyr | Glu |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Arg | Arg | Leu | Leu | Ala | Lys | Ala | Arg | Thr | Val | Pro | Pro | Pro | Pro |
|     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |     |     |

|     |     |     |
|-----|-----|-----|
| Gly | Cys | Ser |
| 465 |     |     |

&lt;210&gt; 181

&lt;211&gt; 284

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 181

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Arg | Ala | Gly | Pro | Glu | Ala | Ala | Gly | Gln | Gly | Ala | Asp | Ser | Ala | Pro |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Ala | Arg | Val | Phe | Met | Lys | Ser | Val | Lys | Leu | Glu | Trp | Val | Gln | Asp |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Arg | Ala | Ala | Gln | Asp | Leu | Cys | Glu | Glu | Ala | Leu | Arg | His | Tyr |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Asp | Phe | Pro | Lys | Leu | Trp | Met | Met | Lys | Gly | Gln | Ile | Glu | Glu | Gln |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Glu | Met | Met | Glu | Lys | Ala | Arg | Glu | Ala | Tyr | Asn | Gln | Gly | Leu | Lys |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Cys | Pro | His | Ser | Thr | Pro | Leu | Trp | Leu | Leu | Leu | Ser | Arg | Leu | Glu |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Lys | Ile | Gly | Gln | Leu | Thr | Arg | Ala | Arg | Ala | Ile | Leu | Glu | Lys | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Leu | Lys | Asn | Pro | Lys | Asn | Pro | Gly | Leu | Trp | Leu | Glu | Ser | Val | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

000260"69594960

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |     |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----|
| Gln<br>1  | Pro       | Gly       | Ile       | Lys<br>5 | Glu       | Ser       | Ile       | Leu       | Met<br>10 | Lys       | Glu       | Thr       | Gln       | Gly<br>15 | Pro |
| Tyr       | Gly       | Gln       | Gly<br>20 | Phe      | Leu       | Gly       | Gln       | Asp<br>25 | Ser       | His       | Gln       | His       | Ile<br>30 | Thr       | His |
| Val       | Leu       | Leu<br>35 | Gly       | Arg      | Glu       | Lys       | Gln<br>40 | Tyr       | Ile       | Pro       | Val       | Glu<br>45 | Arg       | Ser       | Gln |
| Ser       | Ile<br>50 | Ser       | Gly       | Arg      | Asn       | Val<br>55 | Val       | Lys       | Gly       | Gly       | Arg<br>60 | Cys       | Tyr       | Ala       | Ala |
| Ala<br>65 | Pro       | Ser       | Val       | Pro      | Glu<br>70 | Val       | Ala       | Val       | Ile       | Pro<br>75 |           |           |           |           |     |



<400> 183

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<210> 184
<211> 117
<212> PRT
<213> homo sapiens
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<400> 184

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<210> 185
<211> 143
<212> PRT
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100

<213> homo sapiens

<400> 185

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|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Lys<br>1  | Ser        | Ala        | Ala        | Gln<br>5  | Thr       | Ala        | Met        | Thr        | Thr<br>10 | Pro       | Pro        | Gln        | Thr        | Pro<br>15 | Pro       |
| His       | Pro        | Tyr        | Phe<br>20  | Ile       | Asn       | Arg        | Gln        | Asp<br>25  | Phe       | Pro       | Cys        | Ile        | Leu<br>30  | Leu       | Arg       |
| Ile       | Ser        | Ser<br>35  | Ser        | His       | Ser       | Pro        | Ala<br>40  | Pro        | Ser       | Pro       | Met        | Ser<br>45  | Trp        | Leu       | His       |
| His       | Cys<br>50  | Lys        | Thr        | Asp       | Leu       | Leu<br>55  | Gln        | Gly        | Ser       | Gln       | Lys<br>60  | Leu        | Leu        | Leu       | Ala       |
| Leu<br>65 | Tyr        | His        | Phe        | Tyr       | Pro<br>70 | His        | Leu        | Pro        | Pro       | Glu<br>75 | Thr        | Ala        | Thr        | Ile       | His<br>80 |
| Ser       | His        | Cys        | Pro        | Ser<br>85 | Ala       | Leu        | Arg        | Pro        | Ser<br>90 | Ser       | Arg        | Ala        | Asp        | Gly<br>95 | Ser       |
| Met       | Val        | Ile        | Leu<br>100 | Ser       | Trp       | Val        | Val        | Leu<br>105 | Leu       | Lys       | Pro        | Ser        | Gln<br>110 | Gly       | Ala       |
| Asp       | Ser        | Gln<br>115 | Arg        | Ala       | Ser       | Arg        | Val<br>120 | Ser        | Gly       | Leu       | Asp        | Asp<br>125 | Ser        | Lys       | Glu       |
| Gly       | Thr<br>130 | Pro        | Ile        | Phe       | Ile       | Phe<br>135 | Lys        | Thr        | Asp       | Ile       | Pro<br>140 | Arg        | Gly        | Phe       |           |

<210> 186

<211> 84

<212> PRT

<213> homo sapiens

<400> 186

|           |           |           |           |          |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Thr<br>1  | Gln       | Thr       | Arg       | His<br>5 | Phe       | Gln       | Leu       | Ala       | Thr<br>10 | Gln       | Ser       | Gly       | Arg       | Ala<br>15 | Gly       |
| Gly       | Asn       | Thr       | Asp<br>20 | Leu      | Asp       | Ile       | His       | Lys<br>25 | Lys       | Ile       | Lys       | Pro       | Lys<br>30 | Ile       | Lys       |
| His       | Ser       | Ile<br>35 | Leu       | Cys      | Pro       | Leu       | Lys<br>40 | Gly       | Leu       | Ile       | Lys       | Gly<br>45 | Thr       | Gln       | Ser       |
| Pro       | Pro<br>50 | Arg       | Ser       | Pro      | Leu       | Pro<br>55 | Cys       | Gln       | His       | His       | Lys<br>60 | Ala       | Ser       | Ser       | Ala       |
| His<br>65 | Thr       | Lys       | Gly       | Leu      | Gly<br>70 | Arg       | Gly       | Ile       | Leu       | Leu<br>75 | Pro       | Pro       | His       | Gln       | Pro<br>80 |
| Gln       | Glu       | Trp       | Thr       |          |           |           |           |           |           |           |           |           |           |           |           |

000260" 092000

<400> 187

Thr Gln

<400> 188

|           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |           |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Asn<br>1  | Leu       | Ile       | Asn       | Lys<br>5  | Lys       | Lys       | Lys       | His       | Thr<br>10 | Phe       | Leu       | Gln       | Leu       | Val<br>15 | Cys       |
| Ser       | Leu       | Leu       | Val<br>20 | Glu       | Val       | Ile       | Asn       | Arg<br>25 | Phe       | Lys       | Glu       | Lys       | Ile<br>30 | Leu       | Ala       |
| Val       | Asn       | Pro<br>35 | Gln       | Cys       | Leu       | Gln       | Leu<br>40 | Phe       | Trp       | Gln       | Asn       | Ile<br>45 | Phe       | Lys       | Glu       |
| Ile       | Gln<br>50 | Gln       | Ala       | Asn       | Phe       | Glu<br>55 | Val       | Leu       | Met       | Lys       | Val<br>60 | Lys       | Glu       | Gly       | Gly       |
| Ile<br>65 | Ser       | Ser       | Phe       | Gly       | Arg<br>70 | Asn       | Glu       | Lys       | Cys       | Leu<br>75 | Thr       | Arg       | Asp       | Ile       | Thr<br>80 |
| Thr       | His       | Val       | Gly       | Ser<br>85 | Gly       | Cys       | Phe       | Leu       | Pro<br>90 | Lys       | Thr       | Phe       | Arg       | Glu<br>95 | Glu       |

Val Asn

&lt;210&gt; 189

&lt;211&gt; 437

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 189

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Lys<br>1   | Tyr        | Glu        | Leu        | Tyr<br>5   | Thr        | Glu        | Asn        | Ala        | Thr<br>10  | Thr        | Glu        | Lys        | Thr        | Glu<br>15  | Pro        |
| Asn        | Ser        | Gln        | Glu<br>20  | Asp        | Lys        | Asn        | Asp        | Gly<br>25  | Gly        | Lys        | Ser        | Arg        | Lys<br>30  | Gly        | Asn        |
| Ile        | Glu        | Leu<br>35  | Ala        | Ser        | Ser        | Glu        | Pro<br>40  | Gln        | His        | Phe        | Thr        | Thr<br>45  | Thr        | Val        | Thr        |
| Arg        | Cys<br>50  | Ser        | Pro        | Thr        | Val        | Ala<br>55  | Phe        | Val        | Glu        | Phe        | Pro<br>60  | Ser        | Ser        | Pro        | Gln        |
| Leu<br>65  | Lys        | Asn        | Asp        | Val        | Ser<br>70  | Glu        | Glu        | Lys        | Asp        | Gln<br>75  | Lys        | Lys        | Pro        | Glu        | Asn<br>80  |
| Glu        | Met        | Ser        | Gly        | Lys<br>85  | Val        | Glu        | Leu        | Val        | Leu<br>90  | Ser        | Gln        | Lys        | Val        | Val<br>95  | Lys        |
| Pro        | Lys        | Ser        | Pro<br>100 | Glu        | Pro        | Glu        | Ala        | Thr<br>105 | Leu        | Thr        | Phe        | Pro        | Phe<br>110 | Leu        | Asp        |
| Lys        | Met        | Pro<br>115 | Glu        | Ala        | Asn        | Gln        | Leu<br>120 | His        | Leu        | Pro        | Asn        | Leu<br>125 | Asn        | Ser        | Gln        |
| Val        | Asp<br>130 | Ser        | Pro        | Ser        | Ser        | Glu<br>135 | Lys        | Ser        | Pro        | Val        | Met<br>140 | Thr        | Pro        | Phe        | Lys        |
| Phe<br>145 | Trp        | Ala        | Trp        | Asp        | Pro<br>150 | Glu        | Glu        | Glu        | Arg        | Arg<br>155 | Arg        | Gln        | Glu        | Lys        | Trp<br>160 |
| Gln        | Gln        | Glu        | Gln        | Glu<br>165 | Arg        | Leu        | Leu        | Gln        | Glu<br>170 | Arg        | Tyr        | Gln        | Lys        | Glu<br>175 | Gln        |
| Asp        | Lys        | Leu        | Lys<br>180 | Glu        | Glu        | Trp        | Glu        | Lys<br>185 | Ala        | Gln        | Lys        | Glu        | Val<br>190 | Glu        | Glu        |
| Glu        | Glu        | Arg<br>195 | Arg        | Tyr        | Tyr        | Glu        | Glu<br>200 | Glu        | Arg        | Lys        | Ile        | Ile<br>205 | Glu        | Asp        | Thr        |
| Val        | Val<br>210 | Pro        | Phe        | Thr        | Val        | Ser<br>215 | Ser        | Ser        | Ser        | Ala        | Asp<br>220 | Gln        | Leu        | Ser        | Thr        |

000260" 69594960

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Ser<br>225 | Ser        | Ser        | Met        | Thr        | Glu<br>230 | Gly        | Ser        | Gly        | Thr        | Met<br>235 | Asn        | Lys        | Ile        | Asp        | Leu<br>240 |
| Gly        | Asn        | Cys        | Gln        | Asp<br>245 | Glu        | Lys        | Gln        | Asp        | Arg<br>250 | Arg        | Trp        | Lys        | Lys        | Ser<br>255 | Phe        |
| Gln        | Gly        | Asp        | Asp<br>260 | Ser        | Asp        | Leu        | Leu        | Leu<br>265 | Lys        | Thr        | Arg        | Glu        | Ser<br>270 | Asp        | Arg        |
| Leu        | Glu        | Glu<br>275 | Lys        | Gly        | Ser        | Leu        | Thr<br>280 | Glu        | Gly        | Ala        | Leu        | Ala<br>285 | His        | Ser        | Gly        |
| Asn        | Pro<br>290 | Val        | Ser        | Lys        | Gly        | Val<br>295 | His        | Glu        | Asp        | His        | Gln<br>300 | Leu        | Asp        | Thr        | Glu        |
| Ala<br>305 | Gly        | Ala        | Pro        | His        | Cys<br>310 | Gly        | Thr        | Asn        | Pro        | Gln<br>315 | Leu        | Ala        | Gln        | Asp        | Pro<br>320 |
| Ser        | Gln        | Asn        | Gln        | Gln<br>325 | Thr        | Ser        | Asn        | Pro        | Thr<br>330 | His        | Ser        | Ser        | Glu        | Asp<br>335 | Val        |
| Lys        | Pro        | Lys        | Thr<br>340 | Leu        | Pro        | Leu        | Asp        | Lys<br>345 | Ser        | Ile        | Asn        | His        | Gln<br>350 | Ile        | Glu        |
| Ser        | Pro        | Ser<br>355 | Glu        | Arg        | Arg        | Lys        | Ser<br>360 | Ile        | Ser        | Gly        | Lys        | Lys<br>365 | Leu        | Cys        | Ser        |
| Ser        | Cys<br>370 | Gly        | Leu        | Pro        | Leu        | Gly<br>375 | Lys        | Gly        | Ala        | Ala        | Met<br>380 | Ile        | Ile        | Glu        | Thr        |
| Leu<br>385 | Asn        | Leu        | Tyr        | Phe        | His<br>390 | Ile        | Gln        | Cys        | Phe        | Arg<br>395 | Cys        | Gly        | Ile        | Cys        | Lys<br>400 |
| Gly        | Gln        | Leu        | Gly        | Asp<br>405 | Ala        | Val        | Ser        | Gly        | Thr<br>410 | Asp        | Val        | Arg        | Ile        | Arg<br>415 | Asn        |
| Gly        | Leu        | Leu        | Asn<br>420 | Cys        | Asn        | Asp        | Cys        | Tyr<br>425 | Met        | Arg        | Ser        | Arg        | Ser<br>430 | Ala        | Gly        |
| Gln        | Pro        | Thr<br>435 | Thr        | Leu        |            |            |            |            |            |            |            |            |            |            |            |

&lt;210&gt; 190

&lt;211&gt; 331

&lt;212&gt; PRT

&lt;213&gt; homo sapiens

&lt;400&gt; 190

|          |     |     |     |          |     |     |     |     |           |     |     |     |     |           |     |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|
| Ser<br>1 | Ala | Asn | His | Lys<br>5 | Leu | Glu | Val | Asn | Gly<br>10 | Thr | Asp | Gly | Leu | Ala<br>15 | Pro |
|----------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|-----|-----|-----|-----|-----------|-----|

000260"69594960

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val        | Glu        | Val        | Glu<br>20  | Glu        | Leu        | Leu        | Arg        | Gln<br>25  | Ala        | Ser        | Glu        | Arg        | Asn<br>30  | Ser        | Lys        |
| Ser        | Pro        | Thr<br>35  | Glu        | Tyr        | His        | Glu        | Pro<br>40  | Val        | Tyr        | Ala        | Asn        | Pro<br>45  | Phe        | Tyr        | Arg        |
| Pro        | Thr<br>50  | Thr        | Pro        | Gln        | Arg        | Glu<br>55  | Thr        | Val        | Thr        | Pro        | Gly<br>60  | Pro        | Asn        | Phe        | Gln        |
| Glu<br>65  | Arg        | Ile        | Lys        | Ile        | Lys<br>70  | Thr        | Asn        | Gly        | Leu        | Gly<br>75  | Ile        | Gly        | Val        | Asn        | Glu<br>80  |
| Ser        | Ile        | His        | Asn        | Met<br>85  | Gly        | Asn        | Gly        | Leu        | Ser<br>90  | Glu        | Glu        | Arg        | Gly        | Asn<br>95  | Asn        |
| Phe        | Asn        | His        | Ile<br>100 | Ser        | Pro        | Ile        | Pro        | Pro<br>105 | Val        | Pro        | His        | Pro        | Arg<br>110 | Ser        | Val        |
| Ile        | Gln        | Gln<br>115 | Ala        | Glu        | Glu        | Lys        | Leu<br>120 | His        | Thr        | Pro        | Gln        | Lys<br>125 | Arg        | Leu        | Met        |
| Thr        | Pro<br>130 | Trp        | Glu        | Glu        | Ser        | Asn<br>135 | Val        | Met        | Gln        | Asp        | Lys<br>140 | Asp        | Ala        | Pro        | Ser        |
| Pro<br>145 | Lys        | Pro        | Arg        | Leu        | Ser<br>150 | Pro        | Arg        | Glu        | Thr        | Ile<br>155 | Phe        | Gly        | Lys        | Ser        | Glu<br>160 |
| His        | Gln        | Asn        | Ser        | Ser<br>165 | Pro        | Thr        | Cys        | Gln        | Glu<br>170 | Asp        | Glu        | Glu        | Asp        | Val<br>175 | Arg        |
| Tyr        | Asn        | Ile        | Val<br>180 | His        | Ser        | Leu        | Pro        | Pro<br>185 | Asp        | Ile        | Asn        | Asp        | Thr<br>190 | Glu        | Pro        |
| Val        | Thr        | Met<br>195 | Ile        | Phe        | Met        | Gly        | Tyr<br>200 | Gln        | Gln        | Ala        | Glu        | Asp<br>205 | Ser        | Glu        | Glu        |
| Asp        | Lys<br>210 | Lys        | Phe        | Leu        | Thr        | Gly<br>215 | Tyr        | Asp        | Gly        | Ile        | Ile<br>220 | His        | Ala        | Glu        | Leu        |
| Val<br>225 | Val        | Ile        | Asp        | Asp        | Glu<br>230 | Glu        | Glu        | Glu        | Asp        | Glu<br>235 | Gly        | Glu        | Ala        | Glu        | Lys<br>240 |
| Pro        | Ser        | Tyr        | His        | Pro<br>245 | Ile        | Ala        | Pro        | His        | Ser<br>250 | Gln        | Val        | Tyr        | Gln        | Pro<br>255 | Ala        |
| Lys        | Pro        | Thr        | Pro<br>260 | Leu        | Pro        | Arg        | Lys        | Arg<br>265 | Ser        | Glu        | Ala        | Ser        | Pro<br>270 | His        | Glu        |

000260" 59594950

|            |            |            |     |            |            |            |            |     |            |            |            |            |     |     |            |
|------------|------------|------------|-----|------------|------------|------------|------------|-----|------------|------------|------------|------------|-----|-----|------------|
| Asn        | Thr        | Asn<br>275 | His | Lys        | Ser        | Pro        | His<br>280 | Lys | Asn        | Ser        | Ile        | Ser<br>285 | Leu | Lys | Glu        |
| Gln        | Glu<br>290 | Glu        | Ser | Leu        | Gly        | Ser<br>295 | Pro        | Val | His        | His        | Ser<br>300 | Pro        | Phe | Asp | Ala        |
| Gln<br>305 | Thr        | Thr        | Gly | Asp        | Gly<br>310 | Thr        | Glu        | Asp | Pro        | Ser<br>315 | Leu        | Thr        | Ala | Leu | Arg<br>320 |
| Met        | Arg        | Met        | Ala | Lys<br>325 | Leu        | Gly        | Lys        | Lys | Val<br>330 | Ile        |            |            |     |     |            |

<210> 191  
 <211> 216  
 <212> PRT  
 <213> homo sapiens

<400> 191

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu<br>1   | Ser        | Leu        | Thr        | Ser<br>5   | Arg        | Met        | Glu        | Glu        | Ala<br>10  | Glu        | Leu        | Val        | Lys        | Gly<br>15  | Arg        |
| Leu        | Gln        | Ala        | Ile<br>20  | Thr        | Asp        | Lys        | Arg        | Lys<br>25  | Ile        | Gln        | Glu        | Glu        | Ile<br>30  | Ser        | Gln        |
| Lys        | Arg        | Leu<br>35  | Lys        | Ile        | Glu        | Glu        | Asp<br>40  | Lys        | Leu        | Lys        | His        | Gln<br>45  | His        | Leu        | Lys        |
| Lys        | Lys<br>50  | Ala        | Leu        | Arg        | Glu        | Lys<br>55  | Trp        | Leu        | Leu        | Asp        | Gly<br>60  | Ile        | Ser        | Ser        | Gly        |
| Lys<br>65  | Glu        | Gln        | Glu        | Glu        | Met<br>70  | Lys        | Lys        | Gln        | Asn        | Gln<br>75  | Gln        | Asp        | Gln        | His        | Gln<br>80  |
| Ile        | Gln        | Val        | Leu        | Glu<br>85  | Gln        | Ser        | Ile        | Leu        | Arg<br>90  | Leu        | Glu        | Lys        | Glu        | Ile<br>95  | Gln        |
| Asp        | Leu        | Glu        | Lys<br>100 | Ala        | Glu        | Leu        | Gln        | Ile<br>105 | Ser        | Thr        | Lys        | Glu        | Glu<br>110 | Ala        | Ile        |
| Leu        | Lys        | Lys<br>115 | Leu        | Lys        | Ser        | Ile        | Glu<br>120 | Arg        | Thr        | Thr        | Glu        | Asp<br>125 | Ile        | Ile        | Arg        |
| Ser        | Val<br>130 | Lys        | Val        | Glu        | Arg        | Glu<br>135 | Glu        | Arg        | Ala        | Glu        | Glu<br>140 | Ser        | Ile        | Glu        | Asp        |
| Ile<br>145 | Tyr        | Ala        | Asn        | Ile        | Pro<br>150 | Asp        | Leu        | Pro        | Lys        | Ser<br>155 | Tyr        | Ile        | Pro        | Ser        | Arg<br>160 |
| Leu        | Arg        | Lys        | Glu        | Ile<br>165 | Asn        | Glu        | Glu        | Lys        | Glu<br>170 | Asp        | Asp        | Glu        | Gln        | Asn<br>175 | Arg        |

000260"69594960

|     |     |     |     |     |     |     |     |                    |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|--------------------|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Leu | Tyr | Ala | Met | Glu | Ile | <sup>106</sup> Lys | Val | Glu | Lys | Asp | Leu | Lys | Thr |
|     |     |     | 180 |     |     |     |     | 185                |     |     |     |     | 190 |     |     |
| Gly | Glu | Ser | Thr | Val | Leu | Ser | Ser | Asn                | Thr | Ser | Gly | His | Gln | Met | Thr |
|     |     | 195 |     |     |     |     | 200 |                    |     |     |     | 205 |     |     |     |
| Leu | Lys | Gly | Thr | Gly | Val | Lys | Val |                    |     |     |     |     |     |     |     |
|     | 210 |     |     |     |     | 215 |     |                    |     |     |     |     |     |     |     |

<210> 192  
 <211> 290  
 <212> PRT  
 <213> homo sapiens

<400> 192

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Gly | Ala | Gly | Thr | Gln | Pro | Gly | Pro | Leu | Leu | Lys | Lys | Pro | Tyr | Gln |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Pro | Arg | Ile | Lys | Ile | Ser | Lys | Thr | Ser | Val | Asp | Gly | Asp | Pro | His | Phe |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Val | Val | Asp | Phe | Pro | Leu | Ser | Arg | Leu | Thr | Val | Cys | Phe | Asn | Ile | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Gln | Pro | Gly | Asp | Ile | Leu | Arg | Leu | Val | Ser | Asp | His | Arg | Asp | Ser |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Val | Thr | Val | Asn | Gly | Glu | Leu | Ile | Gly | Ala | Pro | Ala | Pro | Pro | Asn |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Gly | His | Lys | Lys | Gln | Arg | Thr | Tyr | Leu | Arg | Thr | Ile | Thr | Ile | Leu | Ile |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asn | Lys | Pro | Glu | Arg | Ser | Tyr | Leu | Glu | Ile | Thr | Pro | Ser | Arg | Val | Ile |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Leu | Asp | Gly | Gly | Asp | Arg | Leu | Val | Leu | Pro | Cys | Asn | Gln | Ser | Val | Val |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Val | Gly | Ser | Trp | Gly | Leu | Glu | Val | Ser | Val | Ser | Ala | Asn | Ala | Asn | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Thr | Val | Thr | Ile | Gln | Gly | Ser | Ile | Ala | Phe | Val | Ile | Leu | Ile | His | Leu |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Tyr | Lys | Lys | Pro | Ala | Pro | Phe | Gln | Arg | His | His | Leu | Gly | Phe | Tyr | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Ala | Asn | Ser | Glu | Gly | Leu | Ser | Ser | Asn | Cys | His | Gly | Leu | Leu | Gly | Gln |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |

000220" 6954559



|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Asn | Gln | Asp | Ala | Arg | Leu | Thr | Glu | Asp | Pro | Ala | Gly | Pro | Ser |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Asn | Leu | Thr | His | Pro | Leu | Leu | Leu | Gln | Val | Gly | Glu | Gly | Pro | Glu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ala | Val | Leu | Thr | Val | Lys | Gly | His | Gln | Val | Pro | Val | Val | Trp | Lys | Gln |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Arg | Lys | Ile | Tyr | Asn | Gly | Glu | Glu | Gln | Ile | Asp | Cys | Trp | Phe | Ala | Arg |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Asn | Asn | Ala | Ala | Lys | Leu | Ile | Asp | Gly | Glu | Tyr | Lys | Asp | Tyr | Leu | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Ser | His | Pro | Phe | Asp | Thr | Gly | Met | Thr | Leu | Gly | Gln | Gly | Met | Ser | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Glu | Leu |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|     | 290 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |

<210> 193  
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 <212> PRT  
 <213> homo sapiens

<400> 193

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | His | Gly | Ser | Tyr | Arg | Thr | Pro | Lys | Arg | Ser | Ser | Thr | Asn | Cys | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Gly | Lys | Phe | Trp | Glu | Leu | Ala | Asp | Ala | Lys | Lys | Lys | Arg | Lys | Lys | Val |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| His | Gln | Lys | Gln | Lys | Arg | Ala | Thr | Ile | Arg | Ala | Thr | Glu | Leu | Ala | Lys |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Lys | Arg | His | Val | Gly | Gly | Ser | Val | Ser | His | Leu | Ser | Pro | Gly | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Val | Lys | Cys | Val | Ile | Thr | Ala | Gln | Val | His | Gly | Lys | Arg | Gln | Gln | Gln |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Lys | Ala | Leu | Cys | Arg | Leu | Glu |     |     |     |     |     |     |     |     |     |
|     |     |     |     | 85  |     |     |     |     |     |     |     |     |     |     |     |

<210> 194  
 <211> 82  
 <212> PRT  
 <213> homo sapiens

<400> 194

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Phe | Ile | Gln | Gly | Met | Cys | Ser | Arg | Lys | Phe | Ala | Trp | Tyr | Leu | Phe |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

000260"6994960

Ile Phe

<400> 195

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Asp<br>1   | Asp        | Arg        | Ser        | His<br>5  | Ala        | Phe        | His        | His        | His<br>10 | Lys        | Ser        | Val        | Ile        | Asp<br>15 | Ala        |
| Met        | Lys        | Gly        | Arg<br>20  | Pro       | Gly        | Gln        | Ser        | Pro<br>25  | Leu       | Phe        | Arg        | Pro        | Ser<br>30  | Gln       | Gly        |
| Thr        | Gly        | Arg<br>35  | Val        | Pro       | Gly        | Thr        | Arg<br>40  | Gln        | Met       | Leu        | Gln        | Asp<br>45  | Ser        | Val       | Gln        |
| Ala        | Ala<br>50  | Leu        | Glu        | Glu       | Val        | Ala<br>55  | Ala        | Ser        | Glu       | Ala        | Leu<br>60  | Leu        | Gly        | Pro       | Leu        |
| Ser<br>65  | Pro        | Pro        | Gly        | Lys       | Ser<br>70  | Arg        | Asp        | Gly        | Asn       | Ala<br>75  | Ser        | Ala        | Gly        | Glu       | Gly<br>80  |
| Cys        | Gln        | Val        | Phe        | Arg<br>85 | Ser        | Pro        | Pro        | Ser        | Glu<br>90 | Val        | Pro        | Ser        | Pro        | Pro<br>95 | Gly        |
| Gln        | Asp        | Thr        | Pro<br>100 | Thr       | Ser        | Thr        | Phe        | Leu<br>105 | Lys       | Arg        | Arg        | Trp        | Asp<br>110 | Ser       | Gln        |
| Val        | Thr        | Leu<br>115 | Leu        | Pro       | Ser        | Lys        | Lys<br>120 | Cys        | Lys       | Ser        | Gln        | Gln<br>125 | Leu        | Gln       | Glu        |
| Ser        | Val<br>130 | Ser        | Gln        | Phe       | Pro        | Pro<br>135 | Ser        | Pro        | Gly       | Gly        | Arg<br>140 | Arg        | Glu        | Gly       | Pro        |
| Trp<br>145 | Ser        | Ser        | Leu        | Gly       | Ala<br>150 | Gly        | Gly        | Pro        | Ser       | Ser<br>155 | His        | Ile        | Ser        | Ala       | Lys<br>160 |



110

Asn Asn Arg Lys Leu  
145

<210> 197  
<211> 143  
<212> PRT  
<213> homo sapiens

<400> 197

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Gly<br>1  | Gln        | Arg        | Cys        | Pro<br>5  | Arg       | Gly        | Thr        | Asp        | Leu<br>10 | Pro       | Glu        | Ala        | Pro        | Thr<br>15 | Leu       |
| Pro       | Leu        | Trp        | Val<br>20  | Asn       | His       | Phe        | Ser        | Pro<br>25  | Gly       | Leu       | Ser        | Leu        | Arg<br>30  | Leu       | His       |
| Gln       | Leu        | Val<br>35  | Gly        | Leu       | Gln       | Ala        | Ser<br>40  | Pro        | Pro       | Asp       | Ser        | Pro<br>45  | His        | Cys       | Trp       |
| Ala       | Thr<br>50  | Leu        | Asn        | Leu       | Lys       | Phe<br>55  | His        | Cys        | Pro       | Ala       | Pro<br>60  | Pro        | Thr        | Pro       | Thr       |
| Pro<br>65 | Lys        | Phe        | Pro        | Lys       | Glu<br>70 | Met        | Ser        | Lys        | Thr       | His<br>75 | Ala        | His        | Thr        | Tyr       | Ile<br>80 |
| His       | Thr        | Cys        | Thr        | Cys<br>85 | Ala       | His        | Thr        | Ser        | Cys<br>90 | Val       | Thr        | Thr        | Gly        | Gln<br>95 | Gly       |
| Asn       | Ala        | Ser        | Leu<br>100 | Arg       | Ile       | Pro        | Gly        | Pro<br>105 | Gly       | Pro       | Gly        | Val        | Lys<br>110 | Gly       | Cys       |
| Ser       | Gly        | Thr<br>115 | Leu        | Pro       | Pro       | Asn        | Leu<br>120 | Leu        | Gly       | Gly       | Pro        | Pro<br>125 | Ser        | Val       | Gly       |
| Ala       | Gly<br>130 | Leu        | Gly        | Val       | Cys       | Leu<br>135 | Asp        | Ser        | Gln       | Asp       | Leu<br>140 | Pro        | Arg        | Ser       |           |

<210> 198  
<211> 142  
<212> PRT  
<213> homo sapiens

<400> 198

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Ser<br>1 | His       | Thr       | Met       | His<br>5 | Cys | Lys       | Glu       | Thr       | Lys<br>10 | Gln | Leu       | Tyr       | Arg       | Ser<br>15 | Gly |
| Asp      | Ala       | Ser       | Val<br>20 | Tyr      | Asn | Thr       | Phe       | Met<br>25 | Ser       | Arg | Ile       | Arg       | Ser<br>30 | Arg       | His |
| Gln      | Asp       | Leu<br>35 | Tyr       | Thr      | Val | Ala       | Ala<br>40 | Ala       | Ile       | Gly | Thr       | Met<br>45 | Ile       | Gln       | Asn |
| Ile      | Lys<br>50 | Tyr       | Ile       | Ser      | Ile | Tyr<br>55 | Ile       | Asn       | Thr       | Gln | Leu<br>60 | Gly       | Trp       | Gly       | Arg |

000260"6994960

111

|           |            |            |            |           |           |            |            |            |           |           |            |            |            |           |           |
|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|------------|------------|------------|-----------|-----------|
| Met<br>65 | Leu        | Gly        | Asp        | Leu       | Val<br>70 | Ser        | Pro        | Ala        | Glu       | Gly<br>75 | Leu        | Gly        | Gly        | Arg       | Glu<br>80 |
| Gly       | Gly        | Gly        | Lys        | Gly<br>85 | Phe       | Leu        | Thr        | Phe        | Val<br>90 | Leu       | Asn        | Asp        | Gly        | Ser<br>95 | Glu       |
| Gly       | Arg        | Arg        | Glu<br>100 | Met       | Gly       | Lys        | His        | Ser<br>105 | Leu       | His       | Thr        | Leu        | Met<br>110 | Cys       | Ser       |
| His       | Thr        | His<br>115 | Ala        | Gln       | Thr       | Lys        | His<br>120 | Arg        | His       | Arg       | Arg        | Val<br>125 | Ser        | Asn       | Ser       |
| Leu       | Thr<br>130 | Leu        | Ile        | Gly       | Lys       | Gln<br>135 | Ala        | Trp        | Asp       | Ile       | Pro<br>140 | Leu        | Gln        |           |           |

<210> 199  
 <211> 189  
 <212> PRT  
 <213> homo sapiens

<400> 199

|            |            |            |            |           |            |            |            |            |           |            |            |            |            |           |            |
|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|------------|------------|------------|-----------|------------|
| Gln<br>1   | Cys        | Arg        | Gly        | Phe<br>5  | Asn        | Leu        | Lys        | Ala        | Tyr<br>10 | Arg        | Asn        | Ala        | Ala        | Glu<br>15 | Ile        |
| Val        | Gln        | Tyr        | Gly<br>20  | Val       | Lys        | Asn        | Asn        | Thr<br>25  | Thr       | Phe        | Leu        | Glu        | Cys<br>30  | Ala       | Pro        |
| Lys        | Ser        | Pro<br>35  | Gln        | Ala       | Ser        | Ile        | Lys<br>40  | Trp        | Leu       | Leu        | Gln        | Lys<br>45  | Asp        | Lys       | Asp        |
| Arg        | Arg<br>50  | Lys        | Glu        | Val       | Lys        | Leu<br>55  | Asn        | Glu        | Arg       | Ile        | Ile<br>60  | Ala        | Thr        | Ser       | Gln        |
| Gly<br>65  | Leu        | Leu        | Ile        | Arg       | Ser<br>70  | Val        | Gln        | Gly        | Ser       | Asp<br>75  | Gln        | Gly        | Leu        | Tyr       | His<br>80  |
| Cys        | Ile        | Ala        | Thr        | Glu<br>85 | Asn        | Ser        | Phe        | Lys        | Gln<br>90 | Thr        | Ile        | Ala        | Lys        | Ile<br>95 | Asn        |
| Phe        | Lys        | Val        | Leu<br>100 | Asp       | Ser        | Glu        | Met        | Val<br>105 | Ala       | Val        | Val        | Thr        | Asp<br>110 | Lys       | Trp        |
| Ser        | Pro        | Trp<br>115 | Thr        | Trp       | Ala        | Ser        | Ser<br>120 | Val        | Arg       | Ala        | Leu        | Pro<br>125 | Phe        | His       | Pro        |
| Lys        | Asp<br>130 | Ile        | Met        | Gly       | Ala        | Phe<br>135 | Ser        | His        | Ser       | Glu        | Met<br>140 | Gln        | Met        | Ile       | Asn        |
| Gln<br>145 | Tyr        | Cys        | Lys        | Asp       | Thr<br>150 | Arg        | Gln        | Gln        | His       | Gln<br>155 | Gln        | Gly        | Asp        | Glu       | Ser<br>160 |

000260"69594960

112

Gln Lys Met Arg Gly Asp Tyr Gly Lys Leu Lys Ala Leu Ile Asn Ser  
165 170 175

Arg Lys Ser Arg Asn Arg Arg Asn Gln Leu Pro Glu Ser  
180 185

<210> 200

<211> 97

<212> PRT

<213> homo sapiens

<400> 200

Phe Phe Arg Glu Ala Glu Ser Pro Phe Val Ala Arg Leu Glu Cys Ser  
1 5 10 15

Gly Ala Ile Ser Ala His Cys Ser Thr Val Ser Ala His Cys Ser Leu  
20 25 30

Arg Pro Pro Val Phe Lys Arg Phe Ser Cys Leu Ser Leu Leu Ser Ser  
35 40 45

Trp Asp Tyr Arg Cys Ala Pro Pro Arg Pro Ala Asn Phe Cys Ile Phe  
50 55 60

Ser Arg Asp Gly Val Ser Leu Cys Trp Pro Gly Trp Ser Gln Ser Arg  
65 70 75 80

Pro Arg Asp Pro Ala His Leu Gly Leu Pro Lys Cys Trp Asp Tyr Arg  
85 90 95

Xxx

<210> 201

<211> 250

<212> PRT

<213> homo sapiens

<400> 201

Glu Thr Arg Val Lys Thr Ser Leu Glu Leu Leu Arg Thr Gln Leu Glu  
1 5 10 15

Pro Thr Gly Thr Val Gly Asn Thr Ile Met Thr Ser Gln Pro Val Pro  
20 25 30

Asn Glu Thr Ile Ile Val Leu Pro Ser Asn Val Ile Asn Phe Ser Gln  
35 40 45

Ala Glu Lys Pro Glu Pro Thr Asn Gln Gly Gln Asp Ser Leu Lys Lys  
50 55 60

His Leu His Ala Glu Ile Lys Val Ile Gly Thr Ile Gln Ile Leu Cys  
65 70 75 80

000260" 9994990

00000000000000000000000000000000

<400> 202

|          |           |           |           |          |     |           |           |           |           |     |           |           |           |           |     |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|
| Glu<br>1 | Lys       | Thr       | Pro       | Gly<br>5 | Phe | Glu       | Trp       | Lys       | Leu<br>10 | Thr | Ala       | Glu       | Ser       | His<br>15 | Arg |
| Pro      | Arg       | Gln       | Gln<br>20 | Gln      | Arg | Gln       | Gln       | Gln<br>25 | Thr       | Phe | Gly       | Ile       | Leu<br>30 | Phe       | Ser |
| Thr      | His       | Val<br>35 | Leu       | Ile      | Ile | His       | Leu<br>40 | Ile       | Ile       | Phe | Leu       | Val<br>45 | Glu       | Lys       | Leu |
| Gln      | Ile<br>50 | Ser       | Leu       | Phe      | Asn | Ile<br>55 | Tyr       | Ile       | Gln       | Phe | Asn<br>60 | Lys       | Pro       | Leu       | Ala |

114

Ser 65 Tyr Leu Phe Ser 70 His Leu Arg Tyr Phe 75 Phe Pro Pro His Leu Ala 80

Pro Val Pro Pro Phe 85 Leu Phe Ser Leu Cys 90 Lys Arg Lys Tyr Leu 95 Thr

Tyr Leu Gly Pro 100 Thr Ser Ile Met

<210> 203

<211> 93

<212> PRT

<213> homo sapiens

<400> 203

His 1 Lys Lys Asn Phe 5 Trp Gln Ile Phe Ile 10 Gln Ile Ala Cys Leu 15 Gln

Trp Gln Ile Ser 20 Gln His Phe Ser Leu 25 Phe Cys Leu Cys Leu 30 Ser Leu

Cys Ile Phe 35 Leu Glu Arg Lys Leu 40 Asn Ala Phe Asn Val 45 Leu Ile Ile

Thr Leu 50 Leu Lys Leu Asp Pro 55 Asn Met Leu Asn Ile 60 Ser Ser Cys Lys

Gly 65 Arg Arg Gly Arg Glu 70 Glu Gln Gly Gln Gly 75 Gly Glu Glu Lys Asn 80

Thr Ser Gly Glu Arg 85 Thr Ser Asn Leu Gln 90 Glu Ala Tyr

<210> 204

<211> 113

<212> PRT

<213> homo sapiens

<400> 204

Arg 1 Pro Lys Pro Gly 5 His Pro Leu Tyr Ser 10 Lys Tyr Met Arg Gly 15 Asp

Val Leu Val Met 20 Leu Lys Gln Thr Glu 25 Asn Asn Tyr Leu Glu 30 Cys Gln

Lys Gly Glu 35 Asp Thr Gly Arg Val 40 His Leu Ser Gln Met 45 Lys Ile Ile

Thr Pro 50 Leu Asp Glu His Leu 55 Arg Ser Arg Pro Asn 60 Asp Pro Ser His

Ala 65 Gln Lys Pro Val Asp 70 Ser Gly Ala Pro His 75 Ala Val Val Leu His 80

000260"6954960





Ile Gly Leu Ser Ser Gly Glu Asp Arg Tyr Arg Leu Val Gln Arg Glu  
100 105 110

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<210> 205
<211> 225
<212> PRT
<213> homo sapiens
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Thr   Ser   Leu   Leu   Glu   Lys   Leu   Val   Tyr   Leu   Leu   Glu   Lys   Ile   Asp   Thr  
1                      5                      10                      15

Asn Tyr Val Lys Val Ile Ile Asp Ile Pro Glu Gly Gly Asn Gly Lys  
35 40 45

Arg Phe Glu Tyr Ile Gly Glu Gln Lys Asp Glu Leu Ser Phe Ser Glu  
65 70 75 80

Gly Glu Ile Ile Ile Leu Lys Glu Tyr Val Asn Glu Glu Trp Ala Arg  
85 90 95

Gly   Glu   Val   Arg  
              100

Gly   Arg   Thr   Gly   Ile   Phe   Pro   Leu   Asn   Phe   Val   Glu  
                        105                        110

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Glu | Asp | Tyr | Pro | Thr | Ser | Gly | Ala | Asn | Val | Leu | Ser | Thr | Lys |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Leu | Lys | Thr | Lys | Lys | Glu | Asp | Ser | Gly | Ser | Asn | Ser | Gln | Val |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |

Asn Ser Leu Pro Ala Glu Trp Cys Glu Ala Leu His Ser Phe Thr Ala  
145 150 155 160

Glu Thr Ser Asp Asp Leu Ser Phe Lys Arg Gly Asp Arg Ile Gln Ile  
165 170 175

Leu Glu Arg Leu Asp Ser Asp Trp Cys Arg Gly Arg Leu Gln Asp Arg  
180 185 190

116

Glu Gly Ile Phe Pro Ala Val Phe Val Arg Pro Cys Pro Ala Glu Ala  
195 200 205

Lys Ser Met Leu Ala Ile Val Pro Lys Gly Gln Glu Gly Gln Ser Leu  
210 215 220

Ile  
225

<210> 206  
<211> 105  
<212> PRT  
<213> homo sapiens

<400> 206

Cys Ile Gly Phe Ser Ser Gly Phe Asp Lys Val Lys Arg Ile Val Thr  
1 5 10 15

Arg Val Thr Gln Thr Cys Gln Leu Ser Glu Ser Leu Val Val Lys Pro  
20 25 30

Glu Leu Gly Lys Leu Ser Leu Arg Arg Leu Lys Glu Arg Ala Gln Val  
35 40 45

Gly Ile Cys Val Ile Thr Val Leu Leu Pro Arg His Gly Val Asp Asn  
50 55 60

Lys Ile Pro Leu Gln Ser Thr Gly Val Ser Val Arg Leu Val Leu Gln  
65 70 75 80

Lys Ala Ala His Trp Glu Trp Gly Gly Ala Cys Gly Lys Pro Asp Cys  
85 90 95

Gly Glu Lys Leu Gly Glu Asn Gly Ser  
100 105

<210> 207  
<211> 83  
<212> PRT  
<213> homo sapiens

<400> 207

Leu Cys Gly Ala Ala Ala Ser Cys Met Met Leu Gly Ser Leu Ala Pro  
1 5 10 15

Asp Pro Gly Ser Arg Arg His Ser Gly Gln Ala Ala Leu Arg Pro Arg  
20 25 30

Arg Tyr Pro Thr Leu Trp Asp Arg Cys Arg Lys Arg Trp Leu Arg Pro  
35 40 45

Ile Phe Thr Gln Leu Leu Ala Ala Val Trp Leu Thr Thr Arg Ser Ser  
50 55 60

000260"69594960



Pro Phe Pro Val Ser Arg Phe Leu Gln His Gln Ala Asn Thr Tyr Thr  
65 70 75 80

Ser Ala Leu

<210> 208

<211> 581

<212> PRT

<213> homo sapiens

<400> 208

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Tyr<br>1   | Phe        | Cys        | Met        | Met<br>5   | Thr        | Glu        | Ala        | Glu        | Gln<br>10  | Asp        | Lys        | Trp        | Gln        | Ala<br>15  | Val        |
| Leu        | Gln        | Asp        | Cys<br>20  | Ile        | Arg        | His        | Cys        | Asn<br>25  | Asn        | Gly        | Ile        | Pro        | Glu<br>30  | Asp        | Ser        |
| Lys        | Val        | Glu<br>35  | Gly        | Pro        | Ala        | Phe        | Thr<br>40  | Asp        | Ala        | Ile        | Arg        | Met<br>45  | Tyr        | Arg        | Gln        |
| Ser        | Lys<br>50  | Glu        | Leu        | Tyr        | Gly        | Thr<br>55  | Trp        | Glu        | Met        | Leu        | Cys<br>60  | Gly        | Asn        | Glu        | Val        |
| Gln<br>65  | Ile        | Leu        | Ser        | Asn        | Leu<br>70  | Val        | Met        | Glu        | Glu        | Leu<br>75  | Gly        | Pro        | Glu        | Leu        | Lys<br>80  |
| Ala        | Glu        | Leu        | Gly        | Pro<br>85  | Arg        | Leu        | Lys        | Gly        | Lys<br>90  | Pro        | Gln        | Glu        | Arg        | Gln<br>95  | Arg        |
| Gln        | Trp        | Ile        | Gln<br>100 | Ile        | Ser        | Asp        | Ala        | Val<br>105 | Tyr        | His        | Met        | Val        | Tyr<br>110 | Glu        | Gln        |
| Ala        | Lys        | Ala<br>115 | Arg        | Phe        | Glu        | Glu        | Val<br>120 | Leu        | Ser        | Lys        | Val        | Gln<br>125 | Gln        | Val        | Gln        |
| Pro        | Ala<br>130 | Met        | Gln        | Ala        | Val        | Ile<br>135 | Arg        | Thr        | Asp        | Met        | Asp<br>140 | Gln        | Ile        | Ile        | Thr        |
| Ser<br>145 | Lys        | Glu        | His        | Leu        | Ala<br>150 | Ser        | Lys        | Ile        | Arg        | Ala<br>155 | Phe        | Ile        | Leu        | Pro        | Lys<br>160 |
| Ala        | Glu        | Val        | Cys        | Val<br>165 | Arg        | Asn        | His        | Val        | Gln<br>170 | Pro        | Tyr        | Ile        | Pro        | Ser<br>175 | Ile        |
| Leu        | Glu        | Ala        | Leu<br>180 | Met        | Val        | Pro        | Thr        | Ser<br>185 | Gln        | Gly        | Phe        | Thr        | Glu<br>190 | Val        | Arg        |
| Asp        | Val        | Phe<br>195 | Phe        | Lys        | Glu        | Val        | Thr<br>200 | Asp        | Met        | Asn        | Leu        | Asn<br>205 | Val        | Ile        | Asn        |

0002250" 69594960

|         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |         |
|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|
| Glu 210 | Gly 210 | Gly 210 | Ile 210 | Asp 210 | Lys 210 | Leu 215 | Gly 215 | Glu 215 | Tyr 215 | Met 215 | Glu 220 | Lys 220 | Leu 220 | Ser 220 | Arg 220 |
| Leu 225 | Ala 225 | Tyr 225 | His 225 | Pro 225 | Leu 230 | Lys 230 | Met 230 | Gln 230 | Ser 230 | Cys 235 | Tyr 235 | Glu 235 | Lys 235 | Met 235 | Glu 240 |
| Ser 245 | Leu 245 | Arg 245 | Leu 245 | Asp 245 | Gly 245 | Leu 245 | Gln 245 | Gln 245 | Arg 250 | Phe 250 | Asp 250 | Val 250 | Ser 255 | Ser 255 | Thr 255 |
| Ser 260 | Val 260 | Phe 260 | Lys 260 | Gln 260 | Arg 260 | Ala 260 | Gln 260 | Ile 265 | His 265 | Met 265 | Arg 265 | Glu 265 | Gln 270 | Met 270 | Asp 270 |
| Asn 275 | Ala 275 | Val 275 | Tyr 275 | Thr 275 | Phe 275 | Glu 275 | Thr 280 | Leu 280 | Leu 280 | His 280 | Gln 280 | Glu 285 | Leu 285 | Gly 285 | Lys 285 |
| Gly 290 | Pro 290 | Thr 290 | Lys 290 | Glu 290 | Glu 290 | Leu 295 | Cys 295 | Lys 295 | Ser 295 | Ile 295 | Gln 300 | Arg 300 | Val 300 | Leu 300 | Glu 300 |
| Arg 305 | Val 305 | Leu 305 | Lys 305 | Lys 305 | Tyr 310 | Asp 310 | Tyr 310 | Asp 310 | Ser 310 | Ser 315 | Ser 315 | Val 315 | Arg 315 | Lys 315 | Arg 320 |
| Phe 325 | Phe 325 | Arg 325 | Glu 325 | Ala 325 | Leu 325 | Leu 325 | Gln 325 | Ile 325 | Ser 330 | Ile 330 | Pro 330 | Phe 330 | Leu 335 | Leu 335 | Lys 335 |
| Lys 340 | Leu 340 | Ala 340 | Pro 340 | Thr 340 | Cys 340 | Lys 340 | Ser 340 | Glu 345 | Leu 345 | Pro 345 | Arg 345 | Phe 345 | Gln 350 | Glu 350 | Leu 350 |
| Ile 355 | Phe 355 | Glu 355 | Asp 355 | Phe 355 | Ala 355 | Arg 355 | Phe 360 | Ile 360 | Leu 360 | Val 360 | Glu 360 | Asn 365 | Thr 365 | Tyr 365 | Glu 365 |
| Glu 370 | Val 370 | Val 370 | Leu 370 | Gln 370 | Thr 370 | Val 375 | Met 375 | Lys 375 | Asp 375 | Ile 375 | Leu 380 | Gln 380 | Ala 380 | Val 380 | Lys 380 |
| Glu 385 | Ala 385 | Ala 385 | Val 385 | Gln 385 | Arg 390 | Lys 390 | His 390 | Asn 390 | Leu 390 | Tyr 395 | Arg 395 | Asp 395 | Ser 395 | Met 395 | Val 400 |
| Met 405 | His 405 | Asn 405 | Ser 405 | Asp 405 | Pro 405 | Asn 405 | Leu 405 | His 405 | Leu 410 | Leu 410 | Ala 410 | Glu 410 | Gly 410 | Ala 415 | Pro 415 |
| Ile 420 | Asp 420 | Trp 420 | Gly 420 | Glu 420 | Glu 420 | Tyr 420 | Ser 420 | Asn 425 | Ser 425 | Gly 425 | Gly 425 | Gly 425 | Gly 430 | Ser 430 | Pro 430 |
| Ala 435 | Pro 435 | Ala 435 | Pro 435 | Arg 435 | Ser 435 | Gln 435 | Pro 440 | Pro 440 | Ser 440 | Arg 440 | Lys 440 | Ser 445 | Asp 445 | Gly 445 | Ala 445 |
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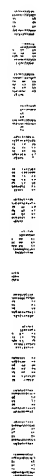
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|------------|------------|------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Leu<br>465 | Arg        | Leu        | Ala        | Leu        | Ser<br>470 | His        | His <sup>119</sup> | His        | Leu        | Arg<br>475 | Pro        | Arg        | Thr        | Val        | Ser<br>480 |
| Leu        | Arg        | Ser        | Glu        | Ala<br>485 | Cys        | Trp        | Pro                | Lys        | Val<br>490 | Cys        | Gly        | Leu        | Arg        | Ala<br>495 | Pro        |
| His        | Gln        | Pro        | Ala<br>500 | Pro        | Cys        | Ser        | Thr                | Gly<br>505 | Pro        | Pro        | Leu        | Gly        | Arg<br>510 | Val        | Pro        |
| Ser        | Leu        | Arg<br>515 | Pro        | Pro        | Pro        | Arg        | Pro<br>520         | Pro        | Arg        | Arg        | Leu        | Pro<br>525 | His        | Pro        | Ser        |
| Ser        | Ile<br>530 | Ser        | Cys        | Leu        | Glu        | Arg<br>535 | Leu                | Trp        | Thr        | Leu        | Gly<br>540 | Pro        | Pro        | Ser        | Pro        |
| Ala<br>545 | Thr        | Arg        | Arg        | Leu        | Glu<br>550 | Ser        | Arg                | Cys        | Pro        | Ala<br>555 | Pro        | Ala        | Ala        | Thr        | Pro<br>560 |
| Pro        | Ser        | Thr        | Pro        | Pro<br>565 | Pro        | Arg        | Thr                | Val        | Gln<br>570 | Gly        | Cys        | Arg        | Leu        | Ser<br>575 | Ser        |
| Arg        | Pro        | Val        | Gly<br>580 | Pro        |            |            |                    |            |            |            |            |            |            |            |            |

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 <211> 466  
 <212> PRT  
 <213> homo sapiens  
 <400> 209

|           |           |           |            |           |           |           |           |            |           |           |           |           |            |           |           |
|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|-----------|-----------|------------|-----------|-----------|
| Pro<br>1  | Gln       | Arg       | Ala        | Ala<br>5  | Pro       | Pro       | Pro       | His        | Pro<br>10 | Gly       | Pro       | Gln       | Arg        | Pro<br>15 | Pro       |
| Ala       | Trp       | Arg       | Ala<br>20  | Val       | Ala       | Phe       | Pro       | Arg<br>25  | Gly       | Trp       | Leu       | Thr       | Pro<br>30  | Gly       | Cys       |
| Trp       | Gly       | Trp<br>35 | Ala        | Ala       | Ala       | Pro       | Ala<br>40 | Ala        | Val       | Ala       | Val       | Leu<br>45 | Leu        | Ala       | Pro       |
| Val       | Asp<br>50 | Gly       | Gly        | Ala       | Leu       | Gly<br>55 | Gln       | Gln        | Val       | Gln       | Val<br>60 | Gly       | Val        | Ala       | Val       |
| Val<br>65 | His       | Asp       | His        | Ala       | Val<br>70 | Pro       | Val       | Glu        | Val       | Val<br>75 | Leu       | Pro       | Leu        | His       | Arg<br>80 |
| Gly       | Leu       | Leu       | His        | Ser<br>85 | Leu       | Gln       | Asp       | Val        | Leu<br>90 | His       | Asp       | Gly       | Leu        | Gln<br>95 | His       |
| His       | Leu       | Leu       | Val<br>100 | Arg       | Val       | Phe       | His       | Gln<br>105 | Asp       | Glu       | Pro       | Gly       | Lys<br>110 | Val       | Leu       |

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| 1990-1991 |  | 1991-1992 |  | 1992-1993 |  | 1993-1994 |  | 1994-1995 |  | 1995-1996 |  | 1996-1997 |  | 1997-1998 |  | 1998-1999 |  | 1999-2000 |  | 2000-2001 |  | 2001-2002 |  | 2002-2003 |  | 2003-2004 |  | 2004-2005 |  | 2005-2006 |  | 2006-2007 |  | 2007-2008 |  | 2008-2009 |  | 2009-2010 |  | 2010-2011 |  | 2011-2012 |  | 2012-2013 |  | 2013-2014 |  | 2014-2015 |  | 2015-2016 |  | 2016-2017 |  | 2017-2018 |  | 2018-2019 |  | 2019-2020 |  | 2020-2021 |  | 2021-2022 |  | 2022-2023 |  | 2023-2024 |  | 2024-2025 |  | 2025-2026 |  | 2026-2027 |  | 2027-2028 |  | 2028-2029 |  | 2029-2030 |  | 2030-2031 |  | 2031-2032 |  | 2032-2033 |  | 2033-2034 |  | 2034-2035 |  | 2035-2036 |  | 2036-2037 |  | 2037-2038 |  | 2038-2039 |  | 2039-2040 |  | 2040-2041 |  | 2041-2042 |  | 2042-2043 |  | 2043-2044 |  | 2044-2045 |  | 2045-2046 |  | 2046-2047 |  | 2047-2048 |  | 2048-2049 |  | 2049-2050 |  | 2050-2051 |  | 2051-2052 |  | 2052-2053 |  | 2053-2054 |  | 2054-2055 |  | 2055-2056 |  | 2056-2057 |  | 2057-2058 |  | 2058-2059 |  | 2059-2060 |  | 2060-2061 |  | 2061-2062 |  | 2062-2063 |  | 2063-2064 |  | 2064-2065 |  | 2065-2066 |  | 2066-2067 |  | 2067-2068 |  | 2068-2069 |  | 2069-2070 |  | 2070-2071 |  | 2071-2072 |  | 2072-2073 |  | 2073-2074 |  | 2074-2075 |  | 2075-2076 |  | 2076-2077 |  | 2077-2078 |  | 2078-2079 |  | 2079-2080 |  | 2080-2081 |  | 2081-2082 |  | 2082-2083 |  | 2083-2084 |  | 2084-2085 |  | 2085-2086 |  | 2086-2087 |  | 2087-2088 |  | 2088-2089 |  | 2089-2090 |  | 2090-2091 |  | 2091-2092 |  | 2092-2093 |  | 2093-2094 |  | 2094-2095 |  | 2095-2096 |  | 2096-2097 |  | 2097-2098 |  | 2098-2099 |  | 2099-2100 |  | 2100-2101 |  | 2101-2102 |  | 2102-2103 |  | 2103-2104 |  | 2104-2105 |  | 2105-2106 |  | 2106-2107 |  | 2107-2108 |  | 2108-2109 |  | 2109-2110 |  | 2110-2111 |  | 2111-2112 |  | 2112-2113 |  | 2113-2114 |  | 2114-2115 |  | 2115-2116 |  | 2116-2117 |  | 2117-2118 |  | 2118-2119 |  | 2119-2120 |  | 2120-2121 |  | 2121-2122 |  | 2122-2123 |  | 2123-2124 |  | 2124-2125 |  | 2125-2126 |  | 2126-2127 |  | 2127-2128 |  | 2128-2129 |  | 2129-2130 |  | 2130-2131 |  | 2131-2132 |  | 2132-2133 |  | 2133-2134 |  | 2134-2135 |  | 2135-2136 |  | 2136-2137 |  | 2137-2138 |  | 2138-2139 |  | 2139-2140 |  | 2140-2141 |  | 2141-2142 |  | 2142-2143 |  | 2143-2144 |  | 2144-2145 |  | 2145-2146 |  | 2146-2147 |  | 2147-2148 |  | 2148-2149 |  | 2149-2150 |  | 2150-2151 |  | 2151-2152 |  | 2152-2153 |  | 2153-2154 |  | 2154-2155 |  | 2155-2156 |  | 2156-2157 |  | 2157-2158 |  | 2158-2159 |  | 2159-2160 |  | 2160-2161 |  | 2161-2162 |  | 2162-2163 |  | 2163-2164 |  | 2164-2165 |  | 2165-2166 |  | 2166-2167 |  | 2167-2168 |  | 2168-2169 |  | 2169-2170 |  | 2170-2171 |  | 2171-2172 |  | 2172-2173 |  | 2173-2174 |  | 2174-2175 |  | 2175-2176 |  | 2176-2177 |  | 2177-2178 |  | 2178-2179 |  | 2179-2180 |  | 2180-2181 |  | 2181-2182 |  | 2182-2183 |  | 2183-2184 |  | 2184-2185 |  | 2185-2186 |  | 2186-2187 |  | 2187-2188 |  | 2188-2189 |  | 2189-2190 |  | 2190-2191 |  | 2191-2192 |  | 2192-2193 |  | 2193-2194 |  | 2194-2195 |  | 2195-2196 |  | 2196-2197 |  | 2197-2198 |  | 2198-2199 |  | 2199-2200 |  | 2200-2201 |  | 2201-2202 |  | 2202-2203 |  | 2203-2204 |  | 2204-2205 |  | 2205-2206 |  | 2206-2207 |  | 2207-2208 |  | 2208-2209 |  | 2209-2210 |  | 2210-2211 |  | 2211-2212 |  | 2212-2213 |  | 2213-2214 |  | 2214-2215 |  | 2215-2216 |  | 2216-2217 |  |
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|
|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|-----------|--|





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# Systematic Gene Search in the Incyte LifeSeq Database

Normal tissue  
~50,000 individual ESTs

Tumor tissue  
~50,000 individual ESTs

Priority list  
High

Prostate  
Breast  
Ovary  
Bladder  
Uterus

Iterative assembling  
with  
increasing mismatch

Low

~8,000 contigs  
+  
~25,000 individual sequences

~8,000 contigs  
+  
~25,000 individual sequences

## Comparison of databases

normal tissue-  
specific  
(expected: 100-500)

nonspecifically  
expressed genes

tumor tissue-  
specific  
(expected: 100-500)

Genes of Interest

Figure 1

REPLACEMENT PAGE (RULE 26)

000260"6994960



## Systematische Gen-Suche in der Incyte LifeSeq Datenbank

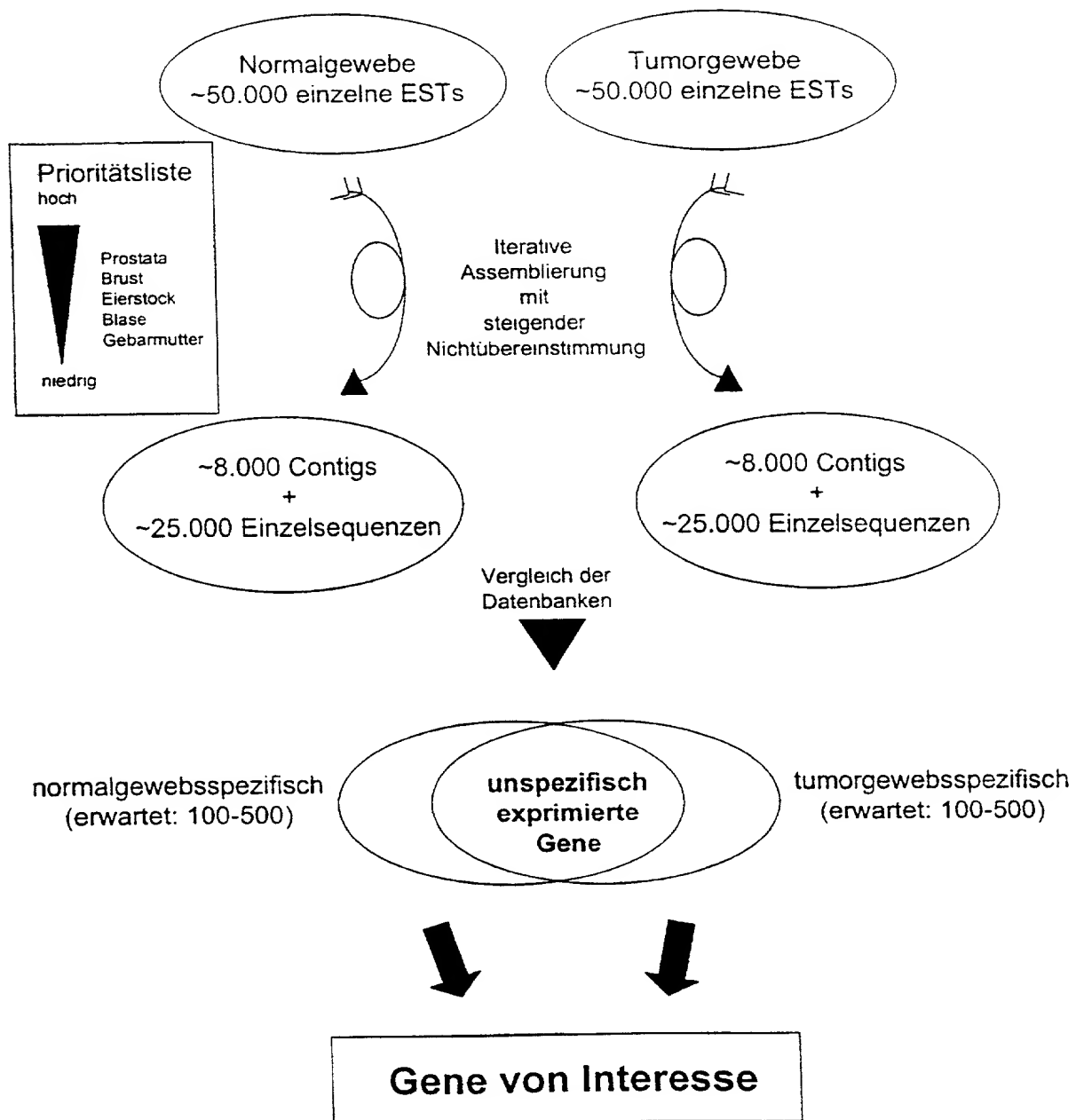


Fig. 1

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## Principle of EST Assembly

~50,000 ESTs per tissue

Assembly at 0% mismatch  
with GAP4 (Staden)

Contigs

Individual Sequences

Contigs increasing in  
number and lengthIterative assembly with  
increasing mismatch  
(1%, 2%, 4%)

5000-6000 contigs

~25,000 other  
individual sequences~30,000 consensus-  
sequences per tissue

Figure 2a

REPLACEMENT PAGE (RULE 26)

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## Prinzip der EST-Assemblierung

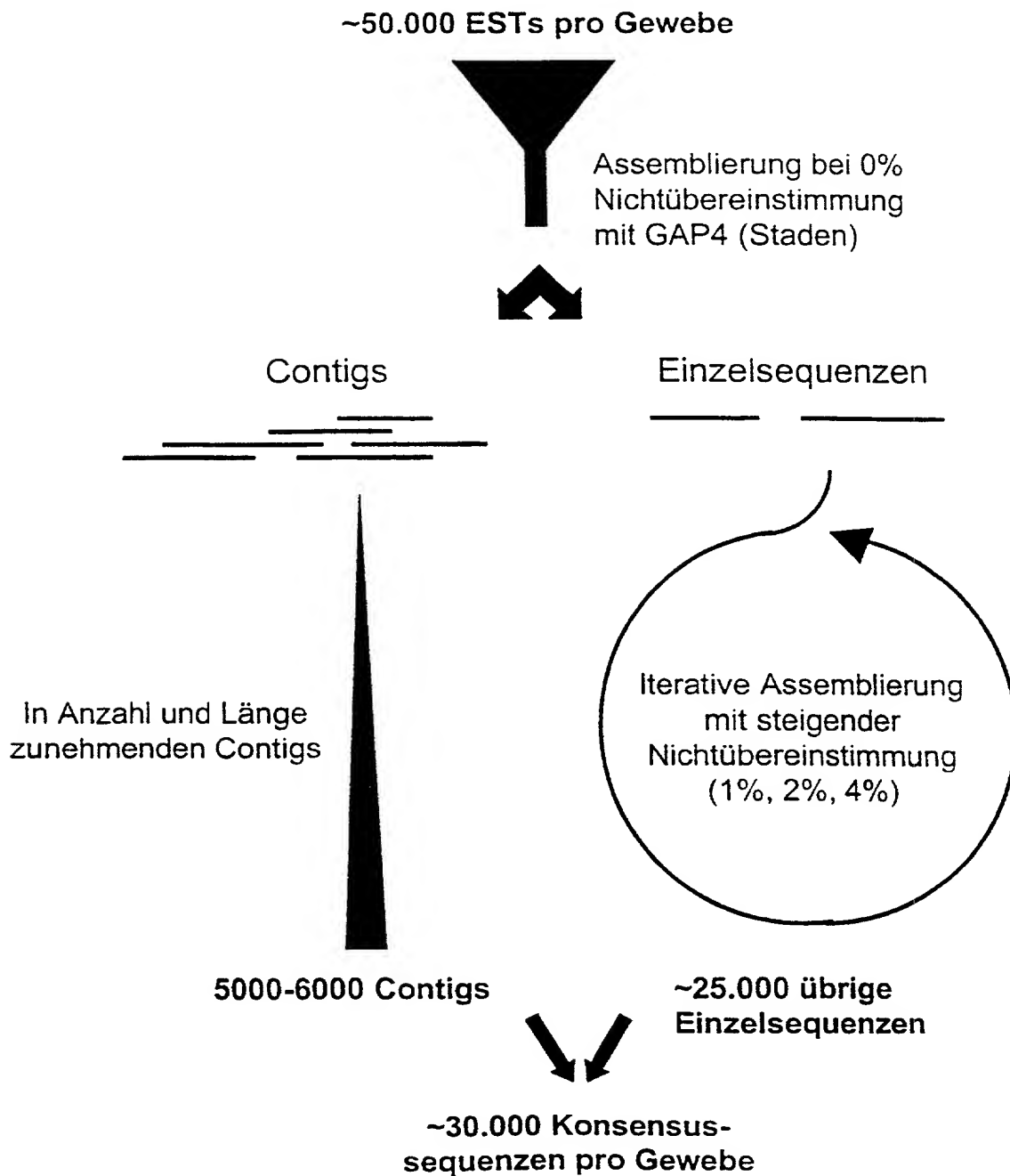


Fig. 2a

~50,000 ESTs of a tissue (e.g.: uterus tumor)

```
GAP4 Assembly 1st Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 0
```

|                        |             |
|------------------------|-------------|
| GAP4 Database 1        | unassembled |
| Contigs 1              | ESTs        |
| Individual sequences 1 |             |

```
GAP4 Assembly 2nd Round:
minimum initial match: 20
maximum number of inserted blanks per
sequence: 8
maximum percent mismatch: 1
```

|                        |             |
|------------------------|-------------|
| GAP4 Database 2        | unassembled |
| Contigs 2              | ESTs        |
| Individual sequences 2 |             |

GAP4 Assembly 3rd Round:  
minimum initial match: 20  
maximum number of inserted blanks per  
sequence: 8  
maximum percent mismatch: 2

```
GAP4 Database 3: unassembled
Contigs 3 ESTs
Individual sequences 3
```

Figure 2b1

[illegible]

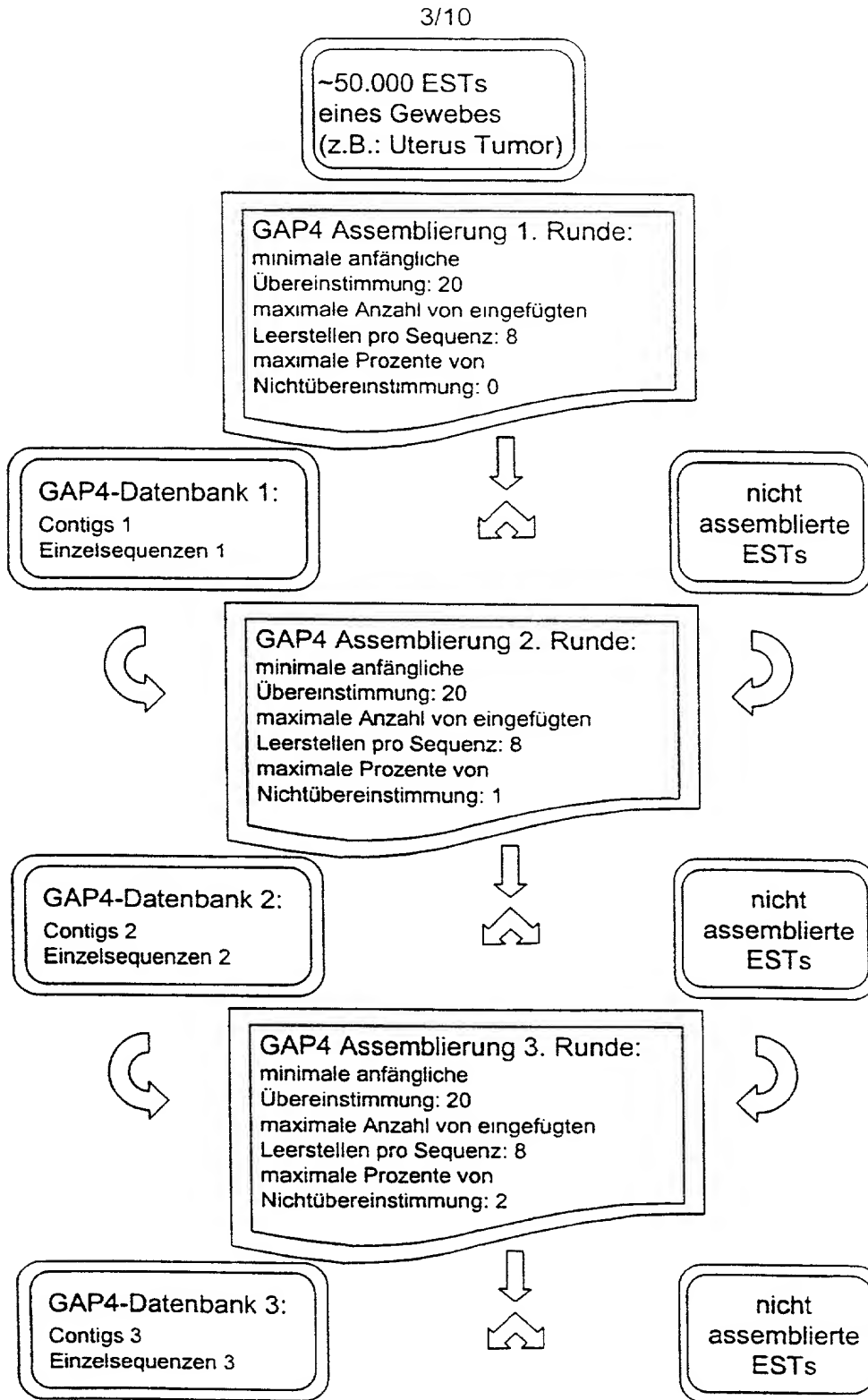


Fig. 2b1

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GAP4 Database 3:  
Contigs 3  
Individual seq. 3

unassembled  
ESTs

Consensus 3

GAP4 Assembly 4th Round:  
minimum initial match: 20  
maximum number of inserted blanks per  
sequence: 8  
maximum percent mismatch: 2

GAP4 Database 4:  
Contigs 4  
Individual seq. 4

unassembled  
ESTs

Consensus 4

GAP4 Assembly 5th Round:  
minimum initial match: 20  
maximum number of inserted blanks per  
sequence: 8  
maximum percent mismatch: 4

GAP4 Database 5:  
Contigs 5  
Individual seq. 5

unassembled  
ESTs 5

Consensus 5

Individual Sequences 5

Figure 2b2

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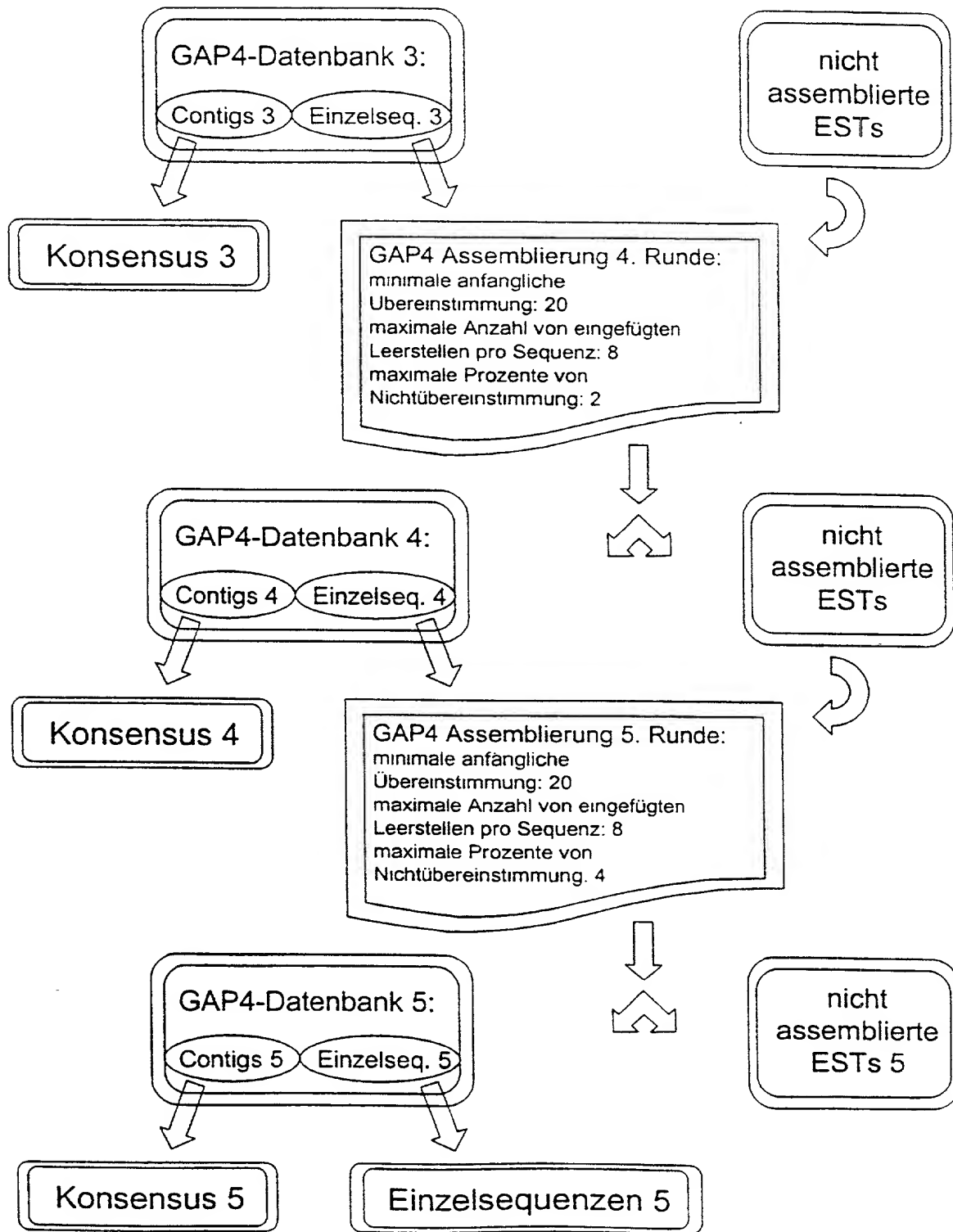


Fig. 2b2

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Consensus 3

Individual Sequences 5

Consensus 4

unassembled  
ESTs 5

Consensus 5

GAP4 Assembly 6th Round:  
minimum initial match: 20  
maximum number of inserted blanks per  
sequence: 8  
maximum percent mismatch: 4

Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Figure 2b3

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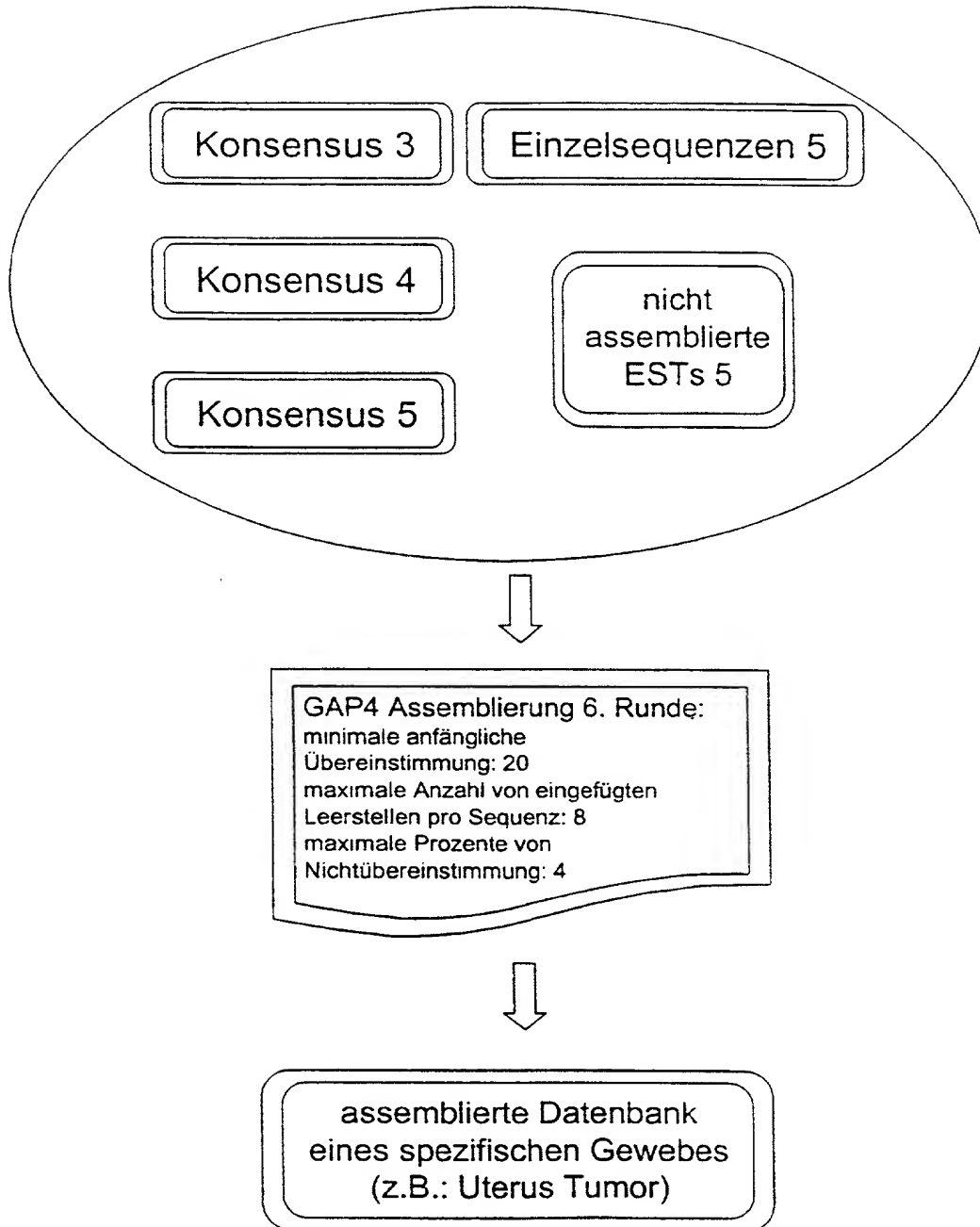


Fig. 2b3

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Assembled database  
of a specific tissue  
(e.g.: uterus tumor)

Consensus 6

Read-in as individual sequences

Database  
of a specific tissue  
(e.g.: uterus tumor)

Database of a second  
specific tissue  
(e.g.: normal uterus)

GAP4 Assembly  
minimum initial match: 20  
maximum number of inserted blanks per  
sequence: 8  
maximum percent mismatch: 4

Tumor tissue-  
specific ESTs

Non-tissue-  
specific ESTs

Normal tissue-  
specific ESTs

Fig. 2b4

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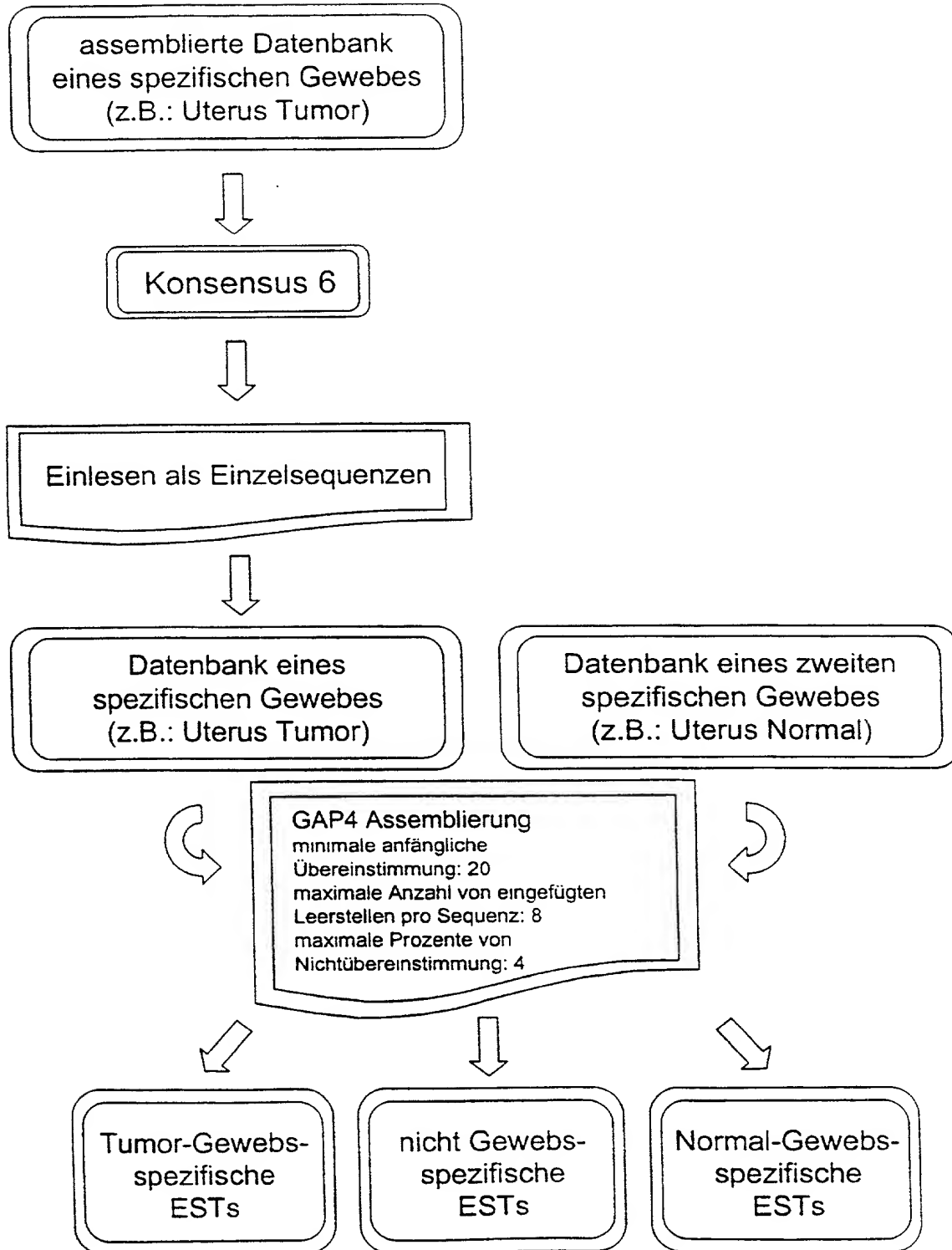


Fig. 2b4

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In silico subtraction of gene expression in various tissues

~30,000 consensus sequences  
normal tissue

~30,000 consensus sequences  
tumor tissue

Assembly at 4% mismatch

Normal tissue  
Specific genes

Cancer tissue  
Specific genes

Genes expressed in both tissues

Figure 3

REPLACEMENT PAGE (RULE 26)

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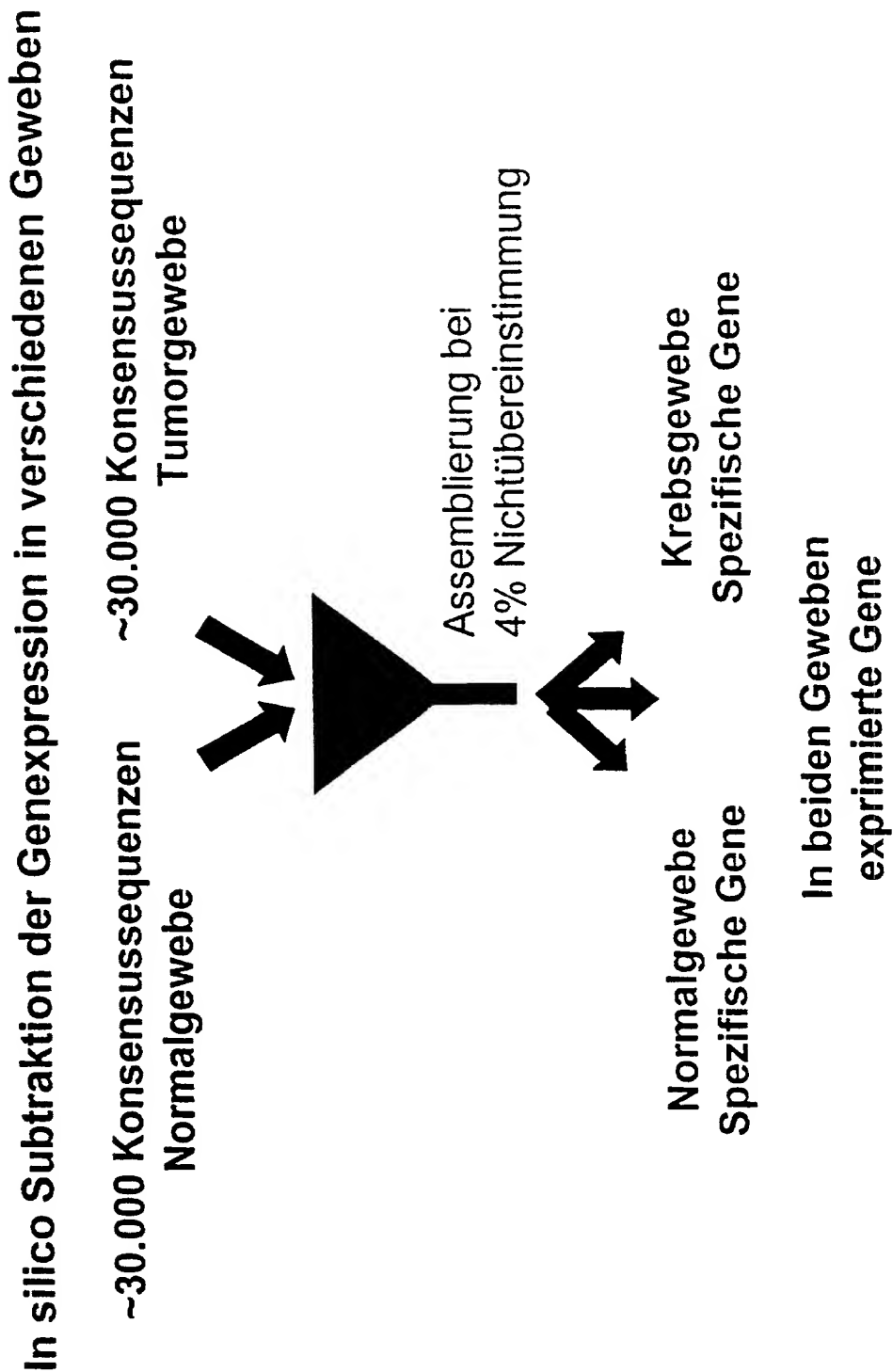


Fig. 3

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Genes of interest

Determination of tissue-specific expression  
via electronic Northern (INCYTE LifeSeq and  
public EST databases)

Candidate genes for tumor suppressors or  
tumor activators

Figure 4a

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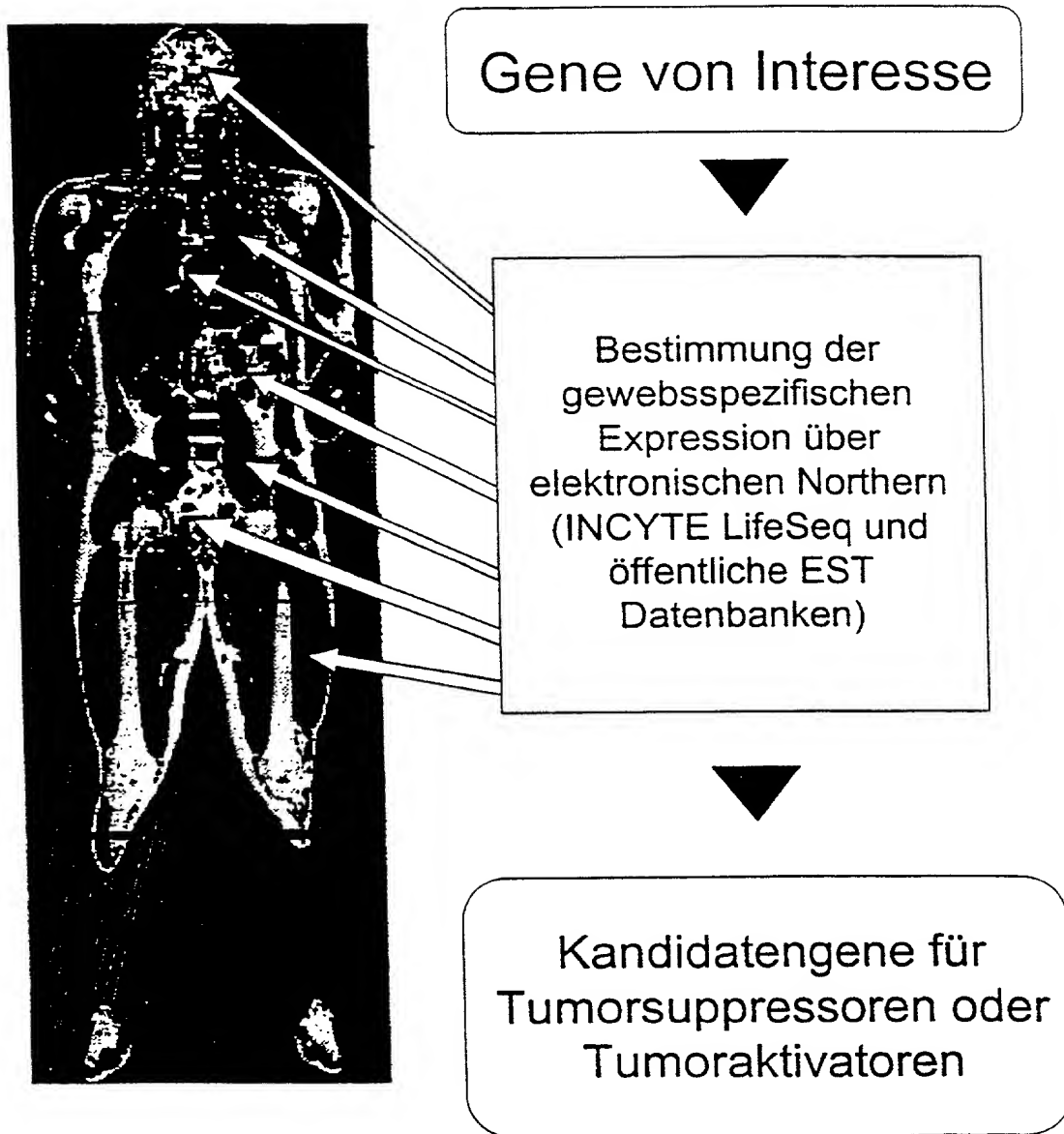


Fig. 4a

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Partial cDNA sequence  
e.g., EST or contig  
S

...GCCTCAAGTTATC...

WHILE  $C_i > C_{i-1}$ 

Electronic Northern Blot

Fisher's Exact Test    IF  $H_0$     EXIT

Automatic Lengthening

Consensus sequence C

...ATGTCCTAGCCTCAAGTTATCAGATGCAA...

Figure 4b

REPLACEMENT PAGE (RULE 26)

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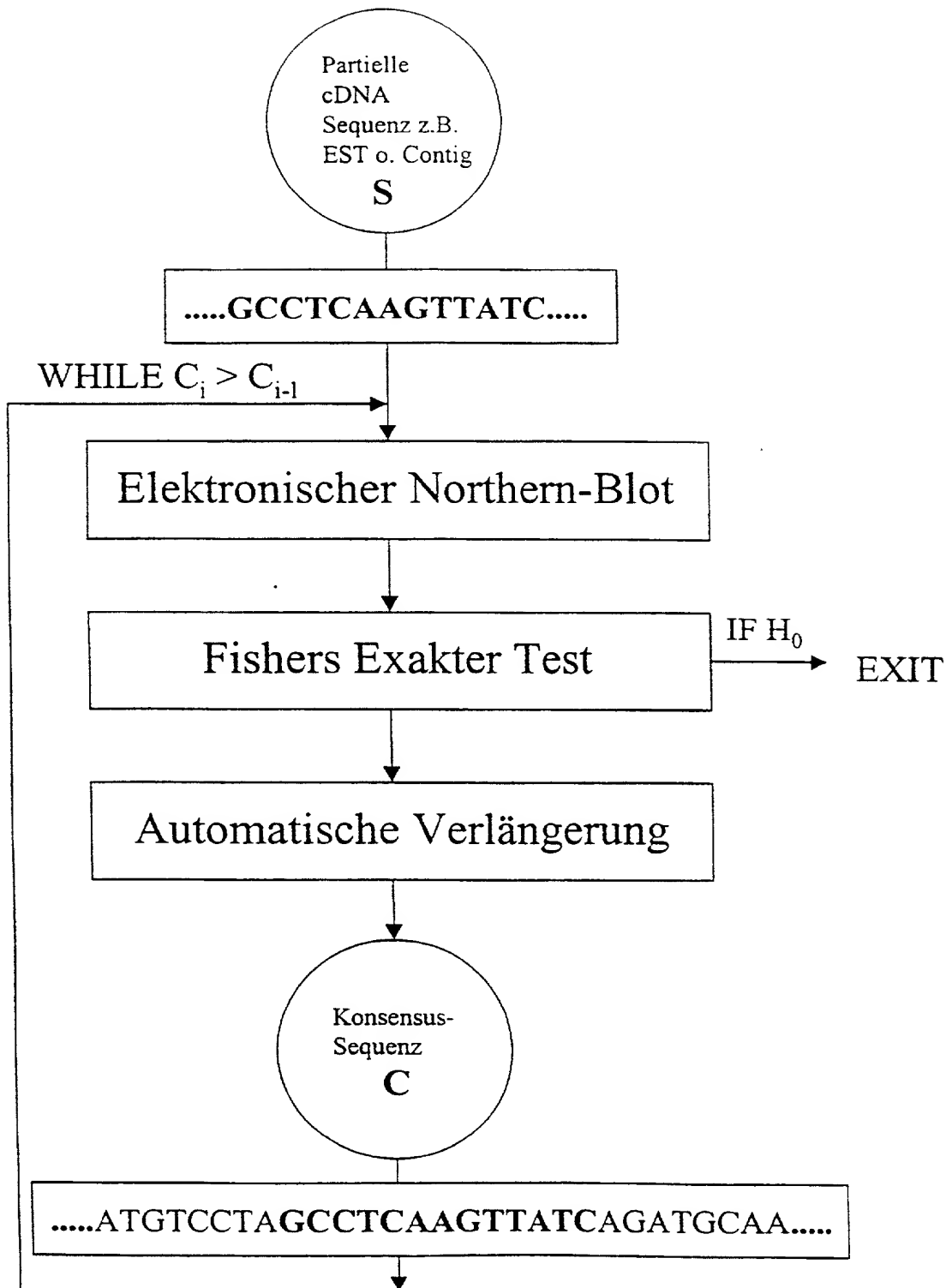


Fig. 4b

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Isolation of genomic BAC and PAC clones

Chromosomal clone localization via FISH

Hybridization signal

Sequencing of clones that are located in regions that have chromosomal deletions in prostate and breast cancer leads to identification of candidate genes

Exon      Intron

Confirmation of candidate genes by screening of mutations and/or deletions in cancer tissues

Figure 5

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Isolieren von genomischen BAC und PAC Klonen



Chromosomale Klon-Lokalisation über FISH



Hybridisierungssignal



Sequenzierung von Klonen, die in Regionen lokalisiert sind, die chromosomale Deletionen in Prostata- und Brustkrebs aufweisen, führt zur Identifizierung von Kandidatengenen



Bestätigung der Kandidatengene durch Screening von Mutationen und/oder Deletionen in Krebsgeweben

Fig. 5